

## SEQUENCE LISTING

<110> Genentech, Inc.  
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Williams, P. Mickey  
Wood, William, I.

<120> Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same

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&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

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Ser	Pro	Gly	Thr	Tyr	Gly	Pro	Asp	Cys	Leu	Ala	Cys	Gln	Gly	Gly	Ser
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Gln Arg Pro Cys Ser Gly Asn Gly His Cys Ser Gly Asp Gly Ser Arg  
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Gln Gly Asp Gly Ser Cys Arg Cys His Met Gly Tyr Gln Gly Pro Leu  
165 170 175

Cys Thr Asp Cys Met Asp Gly Tyr Phe Ser Ser Leu Arg Asn Glu Thr  
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His Ser Ile Cys Thr Ala Cys Asp Glu Ser Cys Lys Thr Cys Ser Gly  
195 200 205

Leu Thr Asn Arg Asp Cys Gly Glu Cys Glu Val Gly Trp Val Leu Asp  
210 215 220

Glu Gly Ala Cys Val Asp Val Asp Glu Cys Ala Ala Glu Pro Pro Pro  
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Cys Ser Ala Ala Gln Phe Cys Lys Asn Ala Asn Gly Ser Tyr Thr Cys  
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Glu Glu Cys Asp Ser Ser Cys Val Gly Cys Thr Gly Glu Gly Pro Gly  
260 265 270

Asn Cys Lys Glu Cys Ile Ser Gly Tyr Ala Arg Glu His Gly Gln Cys  
 275 280 285

Ala Asp Val Asp Glu Cys Ser Leu Ala Glu Lys Thr Cys Val Arg Lys  
290 295 300

Asn Glu Asn Cys Tyr Asn Thr Pro Gly Ser Tyr Val Cys Val Cys Pro  
305 310 315 320

Asp Gly Phe Glu Glu Thr Glu Asp Ala Cys Val Pro Pro Ala Glu Ala  
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<212> DNA

<213> Homo sapiens

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<213> *Homo sapiens*

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Glu Glu Ser Leu Tyr Leu Trp Ile Asp Ala His Gln Ala Arg Val Leu  
35 40 45

Ile Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu Gly Lys Met Ala  
50 55 60

Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln Arg Met Pro Ala Ile

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Pro Val Asn Ile His Ser Met Asn Phe Thr Trp Gln Ala Ala Gly Gln			
85	90	95	
Ala Glu Tyr Phe Tyr Glu Phe Leu Ser Leu Arg Ser Leu Asp Lys Gly			
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Ile Met Ala Asp Pro Thr Val Asn Val Pro Leu Leu Gly Thr Val Pro			
115	120	125	
His Lys Ala Ser Val Val Gln Val Gly Phe Pro Cys Leu Gly Lys Gln			
130	135	140	
Asp Gly Val Ala Ala Phe Glu Val Asp Val Ile Val Met Asn Ser Glu			
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Gly Asn Thr Ile Leu Gln Thr Pro Gln Asn Ala Ile Phe Phe Lys Thr			
165	170	175	
Cys Gln Gln Ala Glu Cys Pro Gly Gly Cys Arg Asn Gly Gly Phe Cys			
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Asn Glu Arg Arg Ile Cys Glu Cys Pro Asp Gly Phe His Gly Pro His			
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Cys Glu Lys Ala Leu Cys Thr Pro Arg Cys Met Asn Gly Gly Leu Cys			
210	215	220	
Val Thr Pro Gly Phe Cys Ile Cys Pro Pro Gly Phe Tyr Gly Val Asn			
225	230	235	240
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Phe Tyr Pro Gly Lys Cys Ile Cys Pro Pro Gly Leu Glu Gly Glu Gln			
260	265	270	
Cys Glu Ile Ser Lys Cys Pro Gln Pro Cys Arg Asn Gly Gly Lys Cys			
275	280	285	
Ile Gly Lys Ser Lys Cys Ser Lys Gly Tyr Gln Gly Asp Leu			
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His Glu Pro Asn Lys Cys Gln Cys Gln Glu Gly Trp His Gly Arg His			
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FID:20020000

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<223> Description of Artificial Sequence: Synthetic  
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<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

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 35 40 45

Gln Glu Gln Asp Leu Cys Cys Arg Gly Arg Ala Asp Asp Cys Ala Leu  
 50 55 60

Pro Tyr Leu Gly Ala Ile Cys Tyr Cys Asp Leu Phe Cys Asn Arg Thr  
 65 70 75 80

Val Ser Asp Cys Cys Pro Asp Phe Trp Asp Phe Cys Leu Gly Val Pro  
 85 90 95

Pro Pro Phe Pro Pro Ile Gln Gly Cys Met His Gly Gly Arg Ile Tyr  
 100 105 110

Pro Val Leu Gly Thr Tyr Trp Asp Asn Cys Asn Arg Cys Thr Cys Gln  
 115 120 125

Glu Asn Arg Gln Trp His Gly Gly Ser Arg His Asp Gln Ser His Gln  
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Pro Gly Gln Leu Trp Leu Ala Gly Trp Glu Pro Gln Arg Leu Leu Gly  
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His Asp Pro Gly

F00720 - E0020000

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<223> a, t, c or g

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<220>
<223> Description of Artificial Sequence: Synthetic
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 35 40 45

Pro Ala Ser Tyr Arg Leu Trp Gly Ala Pro Leu Gln Pro Thr Leu Gly  
 50 55 60

Val Val Pro Gln Ala Ser Val Pro Leu Leu Thr Asp Leu Ala Gln Trp  
 65 70 75 80

Glu Pro Val Leu Val Pro Glu Ala His Pro Asn Ala Ser Leu Thr Met  
 85 90 95

Tyr Val Cys Thr Pro Val Pro His Pro Asp Pro Pro Met Ala Leu Ser  
 100 105 110

Arg Thr Pro Thr Arg Gln Ile Ser Ser Ser Asp Thr Asp Pro Pro Ala  
 115 120 125

Asp Gly Pro Ser Asn Pro Leu Cys Cys Cys Phe His Gly Pro Ala Phe  
 130 135 140

Ser Thr Leu Asn Pro Val Leu Arg His Leu Phe Pro Gln Glu Ala Phe  
 145 150 155 160

Pro Ala His Pro Ile Tyr Asp Leu Ser Gln Val Trp Ser Val Val Ser  
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Pro Ala Pro Ser Arg Gly Gln Ala Leu Arg Arg Ala Gln  
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&lt;210&gt; 19

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

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tgctgtgcta ctcctgcaaa gccc

24

&lt;210&gt; 20

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<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

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<210> 23  
<211> 205  
<212> PRT  
<213> Homo sapiens

&lt;400&gt; 23

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Leu	Ile	Leu	Cys	Cys	Gln	Thr	Gln	Tyr	Val	Arg	Asp	Gln	Gly	Ala	Met
			20					25					30		

Thr	Asp	Gln	Leu	Ser	Arg	Arg	Gln	Ile	Arg	Glu	Tyr	Gln	Leu	Tyr	Ser
				35				40					45		

Arg	Thr	Ser	Gly	Lys	His	Val	Gln	Val	Thr	Gly	Arg	Arg	Ile	Ser	Ala
				50			55					60			

Thr	Ala	Glu	Asp	Gly	Asn	Lys	Phe	Ala	Lys	Leu	Ile	Val	Glu	Thr	Asp
					65		70			75			80		

Thr	Phe	Gly	Ser	Arg	Val	Arg	Ile	Lys	Gly	Ala	Glu	Ser	Glu	Lys	Tyr
					85			90					95		

Ile	Cys	Met	Asn	Lys	Arg	Gly	Lys	Leu	Ile	Gly	Lys	Pro	Ser	Gly	Lys
				100				105				110			

Ser	Lys	Asp	Cys	Val	Phe	Thr	Glu	Ile	Val	Leu	Glu	Asn	Asn	Tyr	Thr
				115			120				125				

Ala	Phe	Gln	Asn	Ala	Arg	His	Glu	Gly	Trp	Phe	Met	Ala	Phe	Thr	Arg
				130			135				140				

Gln	Gly	Arg	Pro	Arg	Gln	Ala	Ser	Arg	Ser	Arg	Gln	Asn	Gln	Arg	Glu
					145		150			155			160		

Ala	His	Phe	Ile	Lys	Arg	Leu	Tyr	Gln	Gly	Gln	Leu	Pro	Phe	Pro	Asn
				165				170				175			

His	Ala	Glu	Lys	Gln	Lys	Gln	Phe	Glu	Phe	Val	Gly	Ser	Ala	Pro	Thr
				180				185				190			

Arg	Arg	Thr	Lys	Arg	Thr	Arg	Arg	Pro	Gln	Pro	Leu	Thr			
				195			200				205				

&lt;210&gt; 24

&lt;211&gt; 28

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 24

cagtacgtga gggaccaggg cgccatga

28

&lt;210&gt; 25

DDBJ  
EMBL  
GenBank

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<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 25
ccggtgacct gcacgtgctt gccca                                         24

<210> 26
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<220>
<221> modified_base
<222> (21)
<223> a, t, c or g

<400> 26
gcggatctgc cgccctgctca nctggtcggt catggcgccc t                                         41

<210> 27
<211> 2479
<212> DNA
<213> Homo sapiens

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ttaccatacg ccctcaggac gttccctcta gctggagttc tggacttcaa cagaacccca 180
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caaatctgcg taagctggaa cggctggata tatccaacaa ccaactgcgg atgctgactc 1140

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 cctcccagaa gtggaaatac aaccggggcc ggcggaaaga tgattattgc gaggcaggca 2040  
 ccaagaagga caactccatc ctggagatga cagaaaccag tttcagatc gtctcctaa 2100  
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<210> 28

<211> 660

<212> PRT

<213> Homo sapiens

<400> 28

Met Gly Leu Gln Thr Thr Lys Trp Pro Ser His Gly Ala Phe Phe Leu

1	5	10	15
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Lys Ser Trp Leu Ile Ile Ser Leu Gly Leu Tyr Ser Gln Val Ser Lys

20	25	30
----	----	----

Leu Leu Ala Cys Pro Ser Val Cys Arg Cys Asp Arg Asn Phe Val Tyr

35	40	45
----	----	----

Cys Asn Glu Arg Ser Leu Thr Ser Val Pro Leu Gly Ile Pro Glu Gly

50	55	60
----	----	----

Val Thr Val Leu Tyr Leu His Asn Asn Gln Ile Asn Asn Ala Gly Phe

65	70	75	80
----	----	----	----

Pro Ala Glu Leu His Asn Val Gln Ser Val His Thr Val Tyr Leu Tyr

85	90	95
----	----	----

Gly Asn Gln Leu Asp Glu Phe Pro Met Asn Leu Pro Lys Asn Val Arg

100	105	110
-----	-----	-----

Val Leu His Leu Gln Glu Asn Asn Ile Gln Thr Ile Ser Arg Ala Ala

115	120	125
-----	-----	-----

Leu Ala Gln Leu Leu Lys Leu Glu Glu Leu His Leu Asp Asp Asn Ser  
 130 135 140  
 Ile Ser Thr Val Gly Val Glu Asp Gly Ala Phe Arg Glu Ala Ile Ser  
 145 150 155 160  
 Leu Lys Leu Leu Phe Leu Ser Lys Asn His Leu Ser Ser Val Pro Val  
 165 170 175  
 Gly Leu Pro Val Asp Leu Gln Glu Leu Arg Val Asp Glu Asn Arg Ile  
 180 185 190  
 Ala Val Ile Ser Asp Met Ala Phe Gln Asn Leu Thr Ser Leu Glu Arg  
 195 200 205  
 Leu Ile Val Asp Gly Asn Leu Leu Thr Asn Lys Gly Ile Ala Glu Gly  
 210 215 220  
 Thr Phe Ser His Leu Thr Lys Leu Lys Glu Phe Ser Ile Val Arg Asn  
 225 230 235 240  
 Ser Leu Ser His Pro Pro Asp Leu Pro Gly Thr His Leu Ile Arg  
 245 250 255  
 Leu Tyr Leu Gln Asp Asn Gln Ile Asn His Ile Pro Leu Thr Ala Phe  
 260 265 270  
 Ser Asn Leu Arg Lys Leu Glu Arg Leu Asp Ile Ser Asn Asn Gln Leu  
 275 280 285  
 Arg Met Leu Thr Gln Gly Val Phe Asp Asn Leu Ser Asn Leu Lys Gln  
 290 295 300  
 Leu Thr Ala Arg Asn Asn Pro Trp Phe Cys Asp Cys Ser Ile Lys Trp  
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 Val Thr Glu Trp Leu Lys Tyr Ile Pro Ser Ser Leu Asn Val Arg Gly  
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 Phe Met Cys Gln Gly Pro Glu Gln Val Arg Gly Met Ala Val Arg Glu  
 340 345 350  
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 355 360 365  
 Leu Phe Thr Pro Ala Pro Ser Thr Ala Ser Pro Thr Thr Gln Pro Pro  
 370 375 380  
 Thr Leu Ser Ile Pro Asn Pro Ser Arg Ser Tyr Thr Pro Pro Thr Pro  
 385 390 395 400  
 Thr Thr Ser Lys Leu Pro Thr Ile Pro Asp Trp Asp Gly Arg Glu Arg

405	410	415
Val Thr Pro Pro Ile Ser Glu Arg Ile Gln Leu Ser Ile His Phe Val		
420	425	430
Asn Asp Thr Ser Ile Gln Val Ser Trp Leu Ser Leu Phe Thr Val Met		
435	440	445
Ala Tyr Lys Leu Thr Trp Val Lys Met Gly His Ser Leu Val Gly Gly		
450	455	460
Ile Val Gln Glu Arg Ile Val Ser Gly Glu Lys Gln His Leu Ser Leu		
465	470	475
Val Asn Leu Glu Pro Arg Ser Thr Tyr Arg Ile Cys Leu Val Pro Leu		
485	490	495
Asp Ala Phe Asn Tyr Arg Ala Val Glu Asp Thr Ile Cys Ser Glu Ala		
500	505	510
Thr Thr His Ala Ser Tyr Leu Asn Asn Gly Ser Asn Thr Ala Ser Ser		
515	520	525
His Glu Gln Thr Thr Ser His Ser Met Gly Ser Pro Phe Leu Leu Ala		
530	535	540
Gly Leu Ile Gly Gly Ala Val Ile Phe Val Leu Val Val Leu Leu Ser		
545	550	555
Val Phe Cys Trp His Met His Lys Lys Gly Arg Tyr Thr Ser Gln Lys		
565	570	575
Trp Lys Tyr Asn Arg Gly Arg Arg Lys Asp Asp Tyr Cys Glu Ala Gly		
580	585	590
Thr Lys Lys Asp Asn Ser Ile Leu Glu Met Thr Glu Thr Ser Phe Gln		
595	600	605
Ile Val Ser Leu Asn Asn Asp Gln Leu Leu Lys Gly Asp Phe Arg Leu		
610	615	620
Gln Pro Ile Tyr Thr Pro Asn Gly Gly Ile Asn Tyr Thr Asp Cys His		
625	630	635
Ile Pro Asn Asn Met Arg Tyr Cys Asn Ser Ser Val Pro Asp Leu Glu		
645	650	655
His Cys His Thr		
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<210> 29		
<211> 21		
<212> DNA		

<213> Artificial Sequence  
<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 29  
cggtctacct gatatggcaac c 21

<210> 30  
<211> 22  
<212> DNA  
<213> Artificial Sequence  
<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 30  
gcaggacaac cagataaacc ac 22

<210> 31  
<211> 22  
<212> DNA  
<213> Artificial Sequence  
<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 31  
acgcagattt gagaaggctg tc 22

<210> 32  
<211> 46  
<212> DNA  
<213> Artificial Sequence  
<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 32  
ttcacgggct gctcttgccc agctcttcaa gcttgaagag ctgcac 46

<210> 33  
<211> 3449  
<212> DNA  
<213> Homo sapiens

<400> 33  
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TOMATO SMOOTHIE

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<210> 34  
 <211> 915  
 <212> PRT  
 <213> Homo sapiens

<400> 34  
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 Ser Arg Gly Arg His Ala Arg Thr His Pro Gln Thr Ala Leu Leu Glu  
 35 40 45  
 Ser Ser Cys Glu Asn Lys Arg Ala Asp Leu Val Phe Ile Ile Asp Ser  
 50 55 60  
 Ser Arg Ser Val Asn Thr His Asp Tyr Ala Lys Val Lys Glu Phe Ile  
 65 70 75 80  
 Val Asp Ile Leu Gln Phe Leu Asp Ile Gly Pro Asp Val Thr Arg Val  
 85 90 95  
 Gly Leu Leu Gln Tyr Gly Ser Thr Val Lys Asn Glu Phe Ser Leu Lys  
 100 105 110  
 Thr Phe Lys Arg Lys Ser Glu Val Glu Arg Ala Val Lys Arg Met Arg  
 115 120 125  
 His Leu Ser Thr Gly Thr Met Thr Gly Leu Ala Ile Gln Tyr Ala Leu  
 130 135 140  
 Asn Ile Ala Phe Ser Glu Ala Glu Gly Ala Arg Pro Leu Arg Glu Asn  
 145 150 155 160  
 Val Pro Arg Val Ile Met Ile Val Thr Asp Gly Arg Pro Gln Asp Ser  
 165 170 175  
 Val Ala Glu Val Ala Ala Lys Ala Arg Asp Thr Gly Ile Leu Ile Phe  
 180 185 190  
 Ala Ile Gly Val Gly Gln Val Asp Phe Asn Thr Leu Lys Ser Ile Gly  
 195 200 205  
 Ser Glu Pro His Glu Asp His Val Phe Leu Val Ala Asn Phe Ser Gln  
 210 215 220  
 Ile Glu Thr Leu Thr Ser Val Phe Gln Lys Lys Leu Cys Thr Ala His

225	230	235	240
Met Cys Ser Thr Leu Glu His Asn Cys Ala His Phe Cys Ile Asn Ile			
245		250	255
Pro Gly Ser Tyr Val Cys Arg Cys Lys Gln Gly Tyr Ile Leu Asn Ser			
260		265	270
Asp Gln Thr Thr Cys Arg Ile Gln Asp Leu Cys Ala Met Glu Asp His			
275		280	285
Asn Cys Glu Gln Leu Cys Val Asn Val Pro Gly Ser Phe Val Cys Gln			
290		295	300
Cys Tyr Ser Gly Tyr Ala Leu Ala Glu Asp Gly Lys Arg Cys Val Ala			
305		310	315
Val Asp Tyr Cys Ala Ser Glu Asn His Gly Cys Glu His Glu Cys Val			
325		330	335
Asn Ala Asp Gly Ser Tyr Leu Cys Gln Cys His Glu Gly Phe Ala Leu			
340		345	350
Asn Pro Asp Glu Lys Thr Cys Thr Arg Ile Asn Tyr Cys Ala Leu Asn			
355		360	365
Lys Pro Gly Cys Glu His Glu Cys Val Asn Met Glu Glu Ser Tyr Tyr			
370		375	380
Cys Arg Cys His Arg Gly Tyr Thr Leu Asp Pro Asn Gly Lys Thr Cys			
385		390	395
Ser Arg Val Asp His Cys Ala Gln Gln Asp His Gly Cys Glu Gln Leu			
405		410	415
Cys Leu Asn Thr Glu Asp Ser Phe Val Cys Gln Cys Ser Glu Gly Phe			
420		425	430
Leu Ile Asn Glu Asp Leu Lys Thr Cys Ser Arg Val Asp Tyr Cys Leu			
435		440	445
Leu Ser Asp His Gly Cys Glu Tyr Ser Cys Val Asn Met Asp Arg Ser			
450		455	460
Phe Ala Cys Gln Cys Pro Glu Gly His Val Leu Arg Ser Asp Gly Lys			
465		470	475
Thr Cys Ala Lys Leu Asp Ser Cys Ala Leu Gly Asp His Gly Cys Glu			
485		490	495
His Ser Cys Val Ser Ser Glu Asp Ser Phe Val Cys Gln Cys Phe Glu			
500		505	510

Gly Tyr Ile Leu Arg Glu Asp Gly Lys Thr Cys Arg Arg Lys Asp Val  
 515 520 525

Cys Gln Ala Ile Asp His Gly Cys Glu His Ile Cys Val Asn Ser Asp  
 530 535 540

Asp Ser Tyr Thr Cys Glu Cys Leu Glu Gly Phe Arg Leu Ala Glu Asp  
 545 550 555 560

Gly Lys Arg Cys Arg Arg Lys Asp Val Cys Lys Ser Thr His His Gly  
 565 570 575

Cys Glu His Ile Cys Val Asn Asn Gly Asn Ser Tyr Ile Cys Lys Cys  
 580 585 590

Ser Glu Gly Phe Val Leu Ala Glu Asp Gly Arg Arg Cys Lys Lys Cys  
 595 600 605

Thr Glu Gly Pro Ile Asp Leu Val Phe Val Ile Asp Gly Ser Lys Ser  
 610 615 620

Leu Gly Glu Glu Asn Phe Glu Val Val Lys Gln Phe Val Thr Gly Ile  
 625 630 635 640

Ile Asp Ser Leu Thr Ile Ser Pro Lys Ala Ala Arg Val Gly Leu Leu  
 645 650 655

Gln Tyr Ser Thr Gln Val His Thr Glu Phe Thr Leu Arg Asn Phe Asn  
 660 665 670

Ser Ala Lys Asp Met Lys Lys Ala Val Ala His Met Lys Tyr Met Gly  
 675 680 685

Lys Gly Ser Met Thr Gly Leu Ala Leu Lys His Met Phe Glu Arg Ser  
 690 695 700

Phe Thr Gln Gly Glu Gly Ala Arg Pro Leu Ser Thr Arg Val Pro Arg  
 705 710 715 720

Ala Ala Ile Val Phe Thr Asp Gly Arg Ala Gln Asp Asp Val Ser Glu  
 725 730 735

Trp Ala Ser Lys Ala Lys Ala Asn Gly Ile Thr Met Tyr Ala Val Gly  
 740 745 750

Val Gly Lys Ala Ile Glu Glu Leu Gln Glu Ile Ala Ser Glu Pro  
 755 760 765

Thr Asn Lys His Leu Phe Tyr Ala Glu Asp Phe Ser Thr Met Asp Glu  
 770 775 780

Ile Ser Glu Lys Leu Lys Lys Gly Ile Cys Glu Ala Leu Glu Asp Ser  
 785 790 795 800

Asp Gly Arg Gln Asp Ser Pro Ala Gly Glu Leu Pro Lys Thr Val Gln  
 805 810 815

Gln Pro Thr Glu Ser Glu Pro Val Thr Ile Asn Ile Gln Asp Leu Leu  
 820 825 830

Ser Cys Ser Asn Phe Ala Val Gln His Arg Tyr Leu Phe Glu Glu Asp  
 835 840 845

Asn Leu Leu Arg Ser Thr Gln Lys Leu Ser His Ser Thr Lys Pro Ser  
 850 855 860

Gly Ser Pro Leu Glu Glu Lys His Asp Gln Cys Lys Cys Glu Asn Leu  
 865 870 875 880

Ile Met Phe Gln Asn Leu Ala Asn Glu Glu Val Arg Lys Leu Thr Gln  
 885 890 895

Arg Leu Glu Glu Met Thr Gln Arg Met Glu Ala Leu Glu Asn Arg Leu  
 900 905 910

Arg Tyr Arg  
 915

<210> 35

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 35

gtgaccctgg ttgtgaatac tcc

23

<210> 36

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 36

acagccatgg tctatagtt gg

22

<210> 37

<211> 45

<212> DNA

<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 37  
gcctgtcagt gtcctgaggg acacgtgctc cgcagcgatg ggaag 45

<210> 38  
<211> 1813  
<212> DNA  
<213> Homo sapiens

<400> 38  
ggagccgccc tgggtgtcag cggctcggtc cccgcgcacg ctccggccgt cgcgacgc 60  
cggcacctgc aggtccgtgc gtccccggc tggegcacct gactccgtcc cggccaggga 120  
ggccatgat ttccctcccg gggcccttgg tgaccactt gctgcggttt ttgttccctgg 180  
ggctgagtgc cctcgcgcgc ccctcgcggg cccagctgca actgcacttg cccgccaacc 240  
ggttcagggc ggtggagggg gggaaagtgg tgcttcagc gtggtaacacc ttgcacgggg 300  
agggttcttc atcccagcca tggaggtgc cctttgtat gtggttcttc aaacagaaaag 360  
aaaaggagga tcaggttttgc tcctacatca atggggtcac aacaagcaaa cctggaggat 420  
ccttggtcta ctccatgccc tcccgaaacc tgcgtcccg gctggagggt ctccaggaga 480  
aagactctgg cccctacagc tgctccgtga atgtcaaga caaacaaggc aaatcttaggg 540  
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gtctccaggg tggccccat gtgggggcaa acgtgaccct gagctgccag tctccaagga 660  
gtaagccgc tgcataac cagtggatc ggcagcttcc atccctccag actttcttg 720  
caccagcatt agatgtcatc cgtgggtctt taagcctcac caacccatcg tcttccatgg 780  
ctggagtcta tgtctgcaag gccacaatg aggtggcac tgcccaatgt aatgtgacgc 840  
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ttggactggg gttgtgttgc gggctgtcc tcttgcacca ccgcggggc aaggccctgg 960  
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ggaaagagtc acactcttgc cccttagtac tctgccttcc cctctcttta ctgtggaaa 1440  
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attggagga gctccaccc accctgact cctccttatg aagccagctg ctgaaatttag 1560  
ctactcacca agagtgggg gcaagactt ccagtcaactg agtctcccttgc gcccccttgc 1620  
tctgtacccc accccatcttcc aacaccaccc ttggctccca ctccagctcc ctgtattgtat 1680  
ataacctgtc aggctggctt ggttaggttt tactggggca gaggataggaaatctttat 1740  
taaaactaac atgaaatatg tggatgttttcc atttgcaaat ttaaataaaag atacataatg 1800  
tttgcataatgaaa 1813

<210> 39  
<211> 390  
<212> PRT  
<213> Homo sapiens

<400> 39  
Met Ile Ser Leu Pro Gly Pro Leu Val Thr Asn Leu Leu Arg Phe Leu

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			20					25						30	
Leu	His	Leu	Pro	Ala	Asn	Arg	Leu	Gln	Ala	Val	Glu	Gly	Gly	Glu	Val
							35			40			45		
Val	Leu	Pro	Ala	Trp	Tyr	Thr	Leu	His	Gly	Glu	Val	Ser	Ser	Ser	Gln
							50			55			60		
Pro	Trp	Glu	Val	Pro	Phe	Val	Met	Trp	Phe	Phe	Lys	Gln	Lys	Glu	Lys
							65			70			75		80
Glu	Asp	Gln	Val	Leu	Ser	Tyr	Ile	Asn	Gly	Val	Thr	Thr	Ser	Lys	Pro
								85			90			95	
Gly	Val	Ser	Leu	Val	Tyr	Ser	Met	Pro	Ser	Arg	Asn	Leu	Ser	Leu	Arg
							100			105			110		
Leu	Glu	Gly	Leu	Gln	Glu	Lys	Asp	Ser	Gly	Pro	Tyr	Ser	Cys	Ser	Val
							115			120			125		
Asn	Val	Gln	Asp	Lys	Gln	Gly	Lys	Ser	Arg	Gly	His	Ser	Ile	Lys	Thr
							130			135			140		
Leu	Glu	Leu	Asn	Val	Leu	Val	Pro	Pro	Ala	Pro	Pro	Ser	Cys	Arg	Leu
							145			150			155		160
Gln	Gly	Val	Pro	His	Val	Gly	Ala	Asn	Val	Thr	Leu	Ser	Cys	Gln	Ser
							165			170			175		
Pro	Arg	Ser	Lys	Pro	Ala	Val	Gln	Tyr	Gln	Trp	Asp	Arg	Gln	Leu	Pro
							180			185			190		
Ser	Phe	Gln	Thr	Phe	Phe	Ala	Pro	Ala	Leu	Asp	Val	Ile	Arg	Gly	Ser
							195			200			205		
Leu	Ser	Leu	Thr	Asn	Leu	Ser	Ser	Ser	Met	Ala	Gly	Val	Tyr	Val	Cys
							210			215			220		
Lys	Ala	His	Asn	Glu	Val	Gly	Thr	Ala	Gln	Cys	Asn	Val	Thr	Leu	Glu
							225			230			235		240
Val	Ser	Thr	Gly	Pro	Gly	Ala	Ala	Val	Val	Ala	Gly	Ala	Val	Val	Gly
							245			250			255		
Thr	Leu	Val	Gly	Leu	Gly	Leu	Leu	Ala	Gly	Leu	Val	Leu	Leu	Tyr	His
							260			265			270		
Arg	Arg	Gly	Lys	Ala	Leu	Glu	Glu	Pro	Ala	Asn	Asp	Ile	Lys	Glu	Asp
							275			280			285		

Ala Ile Ala Pro Arg Thr Leu Pro Trp Pro Lys Ser Ser Asp Thr Ile  
290 295 300

Ser Lys Asn Gly Thr Leu Ser Ser Val Thr Ser Ala Arg Ala Leu Arg  
305 310 315 320

Pro Pro His Gly Pro Pro Arg Pro Gly Ala Leu Thr Pro Thr Pro Ser  
325 330 335

Leu Ser Ser Gln Ala Leu Pro Ser Pro Arg Leu Pro Thr Thr Asp Gly  
340 345 350

Ala His Pro Gln Pro Ile Ser Pro Ile Pro Gly Gly Val Ser Ser Ser  
355 360 365

Gly Leu Ser Arg Met Gly Ala Val Pro Val Met Val Pro Ala Gln Ser  
370 375 380

Gln Ala Gly Ser Leu Val  
385 390

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<210> 40
<211> 22
<212> DNA
<213> Artificial Sequence
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<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 40  
aqqqtctcca qqaqaaaqac tc

22

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<210> 41
<211> 24
<212> DNA
<213> Artificial Sequence
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<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 41  
atttgtqqqcc ttqcaqacat aqac

24

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<210> 42
<211> 50
<212> DNA
<213> Artificial Sequence
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<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

\* \* \* \* \*

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<400> 42
ggccacagca tcaaaaacctt agaactcaat gtactggttc ctccagctcc      50

<210> 43
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 43
gtgtgacaca gcgtgggc      18

<210> 44
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 44
gaccggcagg cttctgcg      18

<210> 45
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 45
cagcagcttc agccaccagg agtgg      25

<210> 46
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 46
ctgagccgtg ggctgcagtc tcgc      24

<210> 47

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<211> 45  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
       oligonucleotide probe  
  
 <400> 47  
 ccgactacga ctggttcttc atcatgcagg atgacacata tgtgc                          45  
  
 <210> 48  
 <211> 2822  
 <212> DNA  
 <213> Homo sapiens  
  
 <400> 48  
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 tggtgaattt ttcctatact caaaaattgca ccaagacacc ttgtctccca aatgcaaaat 120  
 gtgaaatacg caatggatt gaaggctgct attgcaacat ggatttca gaaaaatggtg 180  
 tcacaattt tgaagatgtt aatgaatgtg gaaatttaac tcagtcctgt ggcgaaaatg 240  
 ctaattgcac taacacagaa ggaagtttattt attgtatgtg tgtagctggc ttcagatcca 300  
 gcagtaacca agacagggtt atcaactatg atgaaaccgt ctgtatagaa aatgtaatg 360  
 ccaaactgcca tttagataat gtctgtatag ctgcaaatat taataaaaact ttaacaaaaa 420  
 tcagatccat aaaagaacct gtggctttgc tacaagaagt ctatagaaat tctgtgacag 480  
 atcttcacc aacagatata attacatata tagaaatattt agctgaatca tcttcattac 540  
 tagttacaa gaacaacact atctcagcca aggacaccct ttctactca actcttactg 600  
 aatttgtaaa aaccgtgaat aattttgttc aaaggatac atttgtatgtt tgggacaagt 660  
 tatctgtgaa tcataggaga acacatcttta caaaaactcat gcacactgtt gaacaagcta 720  
 cttaaggat atcccagagc ttccaaaaga ccacagatgtt tgatacaaat tcaacggata 780  
 tagctctcaa agtttcttt tttgattcat ataacatgaa acatattcat cctcatatga 840  
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 gcaatgttgc agttgcattt ttatattata agagtattgg tcctttgctt tcatcatctg 960  
 acaacttctt attgaaacct caaaaattatg ataattctga agaggaggaa agagtcatat 1020  
 cttcagtaat ttctactca atgagctcaa acccaccac attatatgaa cttgaaaaaa 1080  
 taacatttac attaagtcat cgaaaggctca cagatagta taggagtcta tgtgcatttt 1140  
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 agaaacacat ttaccattt tgtgaattgt tctgaactta aatgtccact aaaacaactt 2700  
 agacttctgt ttgctaaatc tggcttttctt tctaataattc taaaaaaaaaaa aaaaagggtt 2760  
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 aa 2822

<210> 49  
 <211> 690  
 <212> PRT  
 <213> Homo sapiens

<400> 49  
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 Cys Glu Ile Arg Asn Gly Ile Glu Ala Cys Tyr Cys Asn Met Gly Phe  
 35 40 45  
 Ser Gly Asn Gly Val Thr Ile Cys Glu Asp Asp Asn Glu Cys Gly Asn  
 50 55 60  
 Leu Thr Gln Ser Cys Gly Glu Asn Ala Asn Cys Thr Asn Thr Glu Gly  
 65 70 75 80  
 Ser Tyr Tyr Cys Met Cys Val Pro Gly Phe Arg Ser Ser Ser Asn Gln  
 85 90 95  
 Asp Arg Phe Ile Thr Asn Asp Gly Thr Val Cys Ile Glu Asn Val Asn  
 100 105 110  
 Ala Asn Cys His Leu Asp Asn Val Cys Ile Ala Ala Asn Ile Asn Lys  
 115 120 125  
 Thr Leu Thr Lys Ile Arg Ser Ile Lys Glu Pro Val Ala Leu Leu Gln  
 130 135 140  
 Glu Val Tyr Arg Asn Ser Val Thr Asp Leu Ser Pro Thr Asp Ile Ile  
 145 150 155 160  
 Thr Tyr Ile Glu Ile Leu Ala Glu Ser Ser Ser Leu Leu Gly Tyr Lys  
 165 170 175  
 Asn Asn Thr Ile Ser Ala Lys Asp Thr Leu Ser Asn Ser Thr Leu Thr

180	185	190
Glu Phe Val Lys Thr Val Asn Asn Phe Val Gln Arg Asp Thr Phe Val		
195	200	205
Val Trp Asp Lys Leu Ser Val Asn His Arg Arg Thr His Leu Thr Lys		
210	215	220
Leu Met His Thr Val Glu Gln Ala Thr Leu Arg Ile Ser Gln Ser Phe		
225	230	235
Gln Lys Thr Thr Glu Phe Asp Thr Asn Ser Thr Asp Ile Ala Leu Lys		
245	250	255
Val Phe Phe Phe Asp Ser Tyr Asn Met Lys His Ile His Pro His Met		
260	265	270
Asn Met Asp Gly Asp Tyr Ile Asn Ile Phe Pro Lys Arg Lys Ala Ala		
275	280	285
Tyr Asp Ser Asn Gly Asn Val Ala Val Ala Phe Leu Tyr Tyr Lys Ser		
290	295	300
Ile Gly Pro Leu Leu Ser Ser Ser Asp Asn Phe Leu Leu Lys Pro Gln		
305	310	315
Asn Tyr Asp Asn Ser Glu Glu Glu Arg Val Ile Ser Ser Val Ile		
325	330	335
Ser Val Ser Met Ser Ser Asn Pro Pro Thr Leu Tyr Glu Leu Glu Lys		
340	345	350
Ile Thr Phe Thr Leu Ser His Arg Lys Val Thr Asp Arg Tyr Arg Ser		
355	360	365
Leu Cys Ala Phe Trp Asn Tyr Ser Pro Asp Thr Met Asn Gly Ser Trp		
370	375	380
Ser Ser Glu Gly Cys Glu Leu Thr Tyr Ser Asn Glu Thr His Thr Ser		
385	390	395
Cys Arg Cys Asn His Leu Thr His Phe Ala Ile Leu Met Ser Ser Gly		
405	410	415
Pro Ser Ile Gly Ile Lys Asp Tyr Asn Ile Leu Thr Arg Ile Thr Gln		
420	425	430
Leu Gly Ile Ile Ile Ser Leu Ile Cys Leu Ala Ile Cys Ile Phe Thr		
435	440	445
Phe Trp Phe Phe Ser Glu Ile Gln Ser Thr Arg Thr Thr Ile His Lys		
450	455	460

Asn Leu Cys Cys Ser Leu Phe Leu Ala Glu Leu Val Phe Leu Val Gly  
 465 470 475 480

Ile Asn Thr Asn Thr Asn Lys Leu Phe Cys Ser Ile Ile Ala Gly Leu  
 485 490 495

Leu His Tyr Phe Phe Leu Ala Ala Phe Ala Trp Met Cys Ile Glu Gly  
 500 505 510

Ile His Leu Tyr Leu Ile Val Val Gly Val Ile Tyr Asn Lys Gly Phe  
 515 520 525

Leu His Lys Asn Phe Tyr Ile Phe Gly Tyr Leu Ser Pro Ala Val Val  
 530 535 540

Val Gly Phe Ser Ala Ala Leu Gly Tyr Arg Tyr Tyr Gly Thr Thr Lys  
 545 550 555 560

Val Cys Trp Leu Ser Thr Glu Asn Asn Phe Ile Trp Ser Phe Ile Gly  
 565 570 575

Pro Ala Cys Leu Ile Ile Leu Val Asn Leu Leu Ala Phe Gly Val Ile  
 580 585 590

Ile Tyr Lys Val Phe Arg His Thr Ala Gly Leu Lys Pro Glu Val Ser  
 595 600 605

Cys Phe Glu Asn Ile Arg Ser Cys Ala Arg Gly Ala Leu Ala Leu Leu  
 610 615 620

Phe Leu Leu Gly Thr Thr Trp Ile Phe Gly Val Leu His Val Val His  
 625 630 635 640

Ala Ser Val Val Thr Ala Tyr Leu Phe Thr Val Ser Asn Ala Phe Gln  
 645 650 655

Gly Met Phe Ile Phe Leu Phe Leu Cys Val Leu Ser Arg Lys Ile Gln  
 660 665 670

Glu Glu Tyr Tyr Arg Leu Phe Lys Asn Val Pro Cys Cys Phe Gly Cys  
 675 680 685

Leu Arg  
 690

<210> 50

<211> 589

<212> DNA

<213> Homo sapiens

<220>

<221> modified\_base

<222> (61)

<223> a, t, c or g

<400> 50

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 ngaaaagccg gcatatggat tcaaattggca atgttgcagt tgcattttta tattataaga 120  
 gtattggtcc ct当地cttc atcatctgac aacttcttat taaaacctca aaattatgat 180  
 aattctgaag aggaggaaag agtcatatct tcagtaattt cagtctcaat gagctcaa 240  
 ccaccacat tataatgact tgaaaaata acatttacat taagtcatcg aaaggcaca 300  
 gataggata ggagtctatg tggcattttg gaataactcac ctgataccat gaatggcago 360  
 tggcttcag agggctgtga gctgacatac tcaaattgaga cccacacctc atgccgtgt 420  
 aatcacctga cacattttgc aattttgatg tcctctggc cttccattgg tattaaagat 480  
 tataatattc ttacaaggat cactcaacta ggaataatta tttcaactgat ttgtcttgcc 540  
 atatgcattt ttaccttctg gttttcagt gaaattcaaa gcaccagga 589

<210> 51

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 51

ggtaatgagc tccattacag

20

<210> 52

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 52

ggagtagaaa gcgcattgg

18

<210> 53

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 53

cacctgatac catgaatggc ag

22

<210> 54

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 54  
cgagctcgaa ttaattcg 18

<210> 55  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 55  
ggatccctg agtcagg 18

<210> 56  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 56  
cctagttgag tgatccttgt aag 23

<210> 57  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 57  
atgagaccca cacctcatgc cgctgtaatc acctgacaca ttttgcatt 50

<210> 58  
<211> 2137  
<212> DNA  
<213> Homo sapiens

<400> 58  
gctcccagcc aagaacctcg gggccgctgc gcgggtgggg aaggttcccc gaaaccggc 60  
cgctaagcga ggcctcctcc tcccgagat ccgaacggcc tgggcggggt caccggct 120

gggacaagaa gccgcccgcct gcctgccccgg gcccggggag ggggctgggg ctggggccgg 180  
 aggcggggtg tgagtgggtg tggcgggggg gcggagacctt gatgcaatcc cgataagaaa 240  
 tgctcggtg tcttgggcac ctaccgggtgg ggcccgttaag gcgtactat ataaggctgc 300  
 cggcccgag ccggccgcgc gtcagagcag gagcgtcgctc tccaggatct agggccacga 360  
 ccatcccaac ccggcactca cagccccgca ggcgcattcccg gtcggccgcggc agcctcccg 420  
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 cgtcggtggac tgcggcgccc gccagagcgc gcacagttt ctggagatca aggcagtcgc 720  
 tctgcggacc gtggccatca agggcgtgca cagcgtgcgg tacctctgca ttggccggca 780  
 cggcaagatg caggggctgc ttcaacttc cggaggaagac tgtgtttcg aggaggagat 840  
 ccccccagat ggctacaatg tgtaccgatc cgagaagcac cgcctccgg tctccctgag 900  
 cagtccaaa cagcggcgc gtcgtacaagaa cagaggctt ctccactct ctcatttcct 960  
 gcccattgtg cccatggcc cagaggagcc tgaggaccc actggccact ttggatctga 1020  
 catgttctct tcgccccctgg agaccgcacat cattggaccca ttgggcttg tcacccggact 1080  
 ggaggccgtg aggagtccca gctttagaaaa gtaactgaga ccatgcccgg gcctttcac 1140  
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 tagcttgcggc agctgtgc tggccccca ttctgtccc tcgagggtgc ttggacaagct 1380  
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 cagaagacag gcagtagttt taatttcagg aacaggtgat ccactctgtaa acacagcagg 1560  
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 cccaggcccc ccaccttatg tcaacctgca ttctgttca aaaaatcagg aaaagaaaag 1920  
 atttgaagac cccaagtctt gtcaataact tgctgtgtgg aagcagcggg ggaagaccta 1980  
 gaacccttcc cccagcactt ggtttccaa catgatattt atgagtaatt tattttgata 2040  
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<210> 59  
 <211> 216  
 <212> PRT  
 <213> Homo sapiens

<400> 59  
 Met Arg Ser Gly Cys Val Val Val His Val Trp Ile Leu Ala Gly Leu  
 1 5 10 15

Trp Leu Ala Val Ala Gly Arg Pro Leu Ala Phe Ser Asp Ala Gly Pro  
 20 25 30

His Val His Tyr Gly Trp Gly Asp Pro Ile Arg Leu Arg His Leu Tyr  
 35 40 45

Thr Ser Gly Pro His Gly Leu Ser Ser Cys Phe Leu Arg Ile Arg Ala  
 50 55 60

Asp Gly Val Val Asp Cys Ala Arg Gly Gln Ser Ala His Ser Leu Leu  
 65                    70                    75                    80

Glu Ile Lys Ala Val Ala Leu Arg Thr Val Ala Ile Lys Gly Val His  
 85                    90                    95

Ser Val Arg Tyr Leu Cys Met Gly Ala Asp Gly Lys Met Gln Gly Leu  
 100                  105                  110

Leu Gln Tyr Ser Glu Glu Asp Cys Ala Phe Glu Glu Glu Ile Arg Pro  
 115                  120                  125

Asp Gly Tyr Asn Val Tyr Arg Ser Glu Lys His Arg Leu Pro Val Ser  
 130                  135                  140

Leu Ser Ser Ala Lys Gln Arg Gln Leu Tyr Lys Asn Arg Gly Phe Leu  
 145                  150                  155                  160

Pro Leu Ser His Phe Leu Pro Met Leu Pro Met Val Pro Glu Glu Pro  
 165                  170                  175

Glu Asp Leu Arg Gly His Leu Glu Ser Asp Met Phe Ser Ser Pro Leu  
 180                  185                  190

Glu Thr Asp Ser Met Asp Pro Phe Gly Leu Val Thr Gly Leu Glu Ala  
 195                  200                  205

Val Arg Ser Pro Ser Phe Glu Lys  
 210                  215

<210> 60

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 60

atccgcccag atggctacaa tgtgta

26

<210> 61

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 61

gcctcccggt ctccctgagc agtgccaaac agcggcagtg ta

42

<210> 62  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 62  
 ccagtccggc gacaagccca aa 22

<210> 63  
 <211> 1295  
 <212> DNA  
 <213> Homo sapiens

<400> 63  
 cccagaagtt caagggcccc cggcctcctg cgctccgtcc gccgggaccc tcgacctcct 60  
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 gctgctgctg cgctacctgg tggcgcctt gggctatcat aaggcctatg gttttctgc 180  
 cccaaaagac caacaagtag tcacagcagt agactaccaa gaggctattt tagcctgcaa 240  
 aaccctaaag aagactgttt cttccagatt agactgaaag aaactgggtc ggagtgtctc 300  
 ctttgtctac tatcaacaga ctcttcaagg tgattttaaa aatcgagctg agatgataga 360  
 ttcaatatac cggatcaaaa atgtgacaag aagtgtatgc gggaaatatac gttgtgaagt 420  
 tagtgccccca tctgagcaag gccaaaaccc ggaagaggat acactcactc tggaaagtatt 480  
 agtggctcca gcagttccat catgtgaagt acccttcttct gctctgagtg gaactgtgg 540  
 agagctacga tgtcaagaca aagaaggaa tccagctcct gaatacacat ggttaagga 600  
 tggcatccgt ttgctagaaa atcccagact tggctccaa agcaccaaca gctcatacac 660  
 aatgaataca aaaactgaa ctctgcaatt taatactgtt tccaaactgg acactggaga 720  
 atattccctgt gaagcccgca attctgttgg atatcgccagg tgcctggaa aacgaatgca 780  
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 ctggcatgg tggcatgtgc ctgcagttcc agctgcttgg gagacaggag aatcacttga 1140  
 accggggagg cggaggttgc agtgagctga gatcacgcca ctgcagtcctt gcctggtaa 1200  
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 tgtagaattt ttacaataaaa tatagtttg tattc 1295

<210> 64  
 <211> 312  
 <212> PRT  
 <213> Homo sapiens

<400> 64  
 Met Ala Arg Arg Ser Arg His Arg Leu Leu Leu Leu Leu Arg Tyr  
 1 5 10 15

Leu Val Val Ala Leu Gly Tyr His Lys Ala Tyr Gly Phe Ser Ala Pro  
 20 25 30

Lys Asp Gln Gln Val Val Thr Ala Val Glu Tyr Gln Glu Ala Ile Leu  
     35                        40                        45

Ala Cys Lys Thr Pro Lys Lys Thr Val Ser Ser Arg Leu Glu Trp Lys  
     50                        55                        60

Lys Leu Gly Arg Ser Val Ser Phe Val Tyr Tyr Gln Gln Thr Leu Gln  
     65                        70                        75                        80

Gly Asp Phe Lys Asn Arg Ala Glu Met Ile Asp Phe Asn Ile Arg Ile  
     85                        90                        95

Lys Asn Val Thr Arg Ser Asp Ala Gly Lys Tyr Arg Cys Glu Val Ser  
     100                       105                       110

Ala Pro Ser Glu Gln Gly Gln Asn Leu Glu Glu Asp Thr Val Thr Leu  
     115                       120                       125

Glu Val Leu Val Ala Pro Ala Val Pro Ser Cys Glu Val Pro Ser Ser  
     130                       135                       140

Ala Leu Ser Gly Thr Val Val Glu Leu Arg Cys Gln Asp Lys Glu Gly  
     145                       150                       155                       160

Asn Pro Ala Pro Glu Tyr Thr Trp Phe Lys Asp Gly Ile Arg Leu Leu  
     165                       170                       175

Glu Asn Pro Arg Leu Gly Ser Gln Ser Thr Asn Ser Ser Tyr Thr Met  
     180                       185                       190

Asn Thr Lys Thr Gly Thr Leu Gln Phe Asn Thr Val Ser Lys Leu Asp  
     195                       200                       205

Thr Gly Glu Tyr Ser Cys Glu Ala Arg Asn Ser Val Gly Tyr Arg Arg  
     210                       215                       220

Cys Pro Gly Lys Arg Met Gln Val Asp Asp Leu Asn Ile Ser Gly Ile  
     225                       230                       235                       240

Ile Ala Ala Val Val Val Ala Leu Val Ile Ser Val Cys Gly Leu  
     245                       250                       255

Gly Val Cys Tyr Ala Gln Arg Lys Gly Tyr Phe Ser Lys Glu Thr Ser  
     260                       265                       270

Phe Gln Lys Ser Asn Ser Ser Lys Ala Thr Thr Met Ser Glu Asn  
     275                       280                       285

Val Gln Trp Leu Thr Pro Val Ile Pro Ala Leu Trp Lys Ala Ala Ala  
     290                       295                       300

Gly Gly Ser Arg Gly Gln Glu Phe

305	310	
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<210> 65
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 65
atcgttgtga agtttagtgcc cc

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22

  

<210> 66		
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<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 66
acctgcgata tccaaacagaaa ttg

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23

  

<210> 67		
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<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 67
ggaagaggat acagtcactc tggaagtatt agtggctcca gcagttcc

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48

  

<210> 68		
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<211> 2639
<212> DNA
<213> Homo sapiens

<400> 68
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gcacatcatgct gctattcctg caaatactga agaagcatgg gatttaaata ttttacttct 180
aaataaatga attactcaat ctcctatgac catctataca tactccacct tcaaaaaagta 240
catcaatatt atatcatcaa ggaatatgtt accttctt ctccaaatgtt catgacattt 300
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tggcattcat catttgcataa atgcaagcat cttccttatac aatcagctcc tattgaactt 420
actagcactg actgtggaaat ccttaagggc ccattacatt tctgaagaag aaagctaaga 480
tgaaggacat gccactccga attcatgtgc tacttggcct agctatcact acactagta 540

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aagctgtaga taaaaaaagtg gattgtccac ggttatgtac gtgtgaaatc aggccttgg 600  
 ttacacccag atccatttat atgaaagcat ctacagtgg a ttgtaatgat ttaggtctt 660  
 taacttccc agccagattg ccagctaaca cacagattct ttcctcacag actaacaata 720  
 ttgcaaaaat tgaatactcc acagacttcc cagtaaacct tactggcctg gatttatctc 780  
 aaaacaattt atttcagtc accaatatta atgtaaaaaa gatgcctcag ctcccttctg 840  
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 gtaagtggtt tgatgcttcc ccaaacttag agattctgat gattggggaa aatccaatta 1080  
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 gtataaacct cacagaataa ccagataacg cttgggtgg actggaaaac ttagaaagca 1200  
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 taaatctctg ggaaggcagga aaagaaaaaa gtacatcact gaaagtaaaa gcaactgtta 2580  
 tagtttacc aacaaatatg tcctaaaaac caccaaggaa acctactcca aaaatgaac 2639

<210> 69  
 <211> 708  
 <212> PRT  
 <213> Homo sapiens

<400> 69  
 Met Lys Asp Met Pro Leu Arg Ile His Val Leu Leu Gly Leu Ala Ile  
 1 5 10 15

Thr Thr Leu Val Gln Ala Val Asp Lys Lys Val Asp Cys Pro Arg Leu  
 20 25 30

Cys Thr Cys Glu Ile Arg Pro Trp Phe Thr Pro Arg Ser Ile Tyr Met  
 35 40 45

Glu Ala Ser Thr Val Asp Cys Asn Asp Leu Gly Leu Leu Thr Phe Pro  
 50 55 60

Ala Arg Leu Pro Ala Asn Thr Gln Ile Leu Leu Leu Gln Thr Asn Asn  
 65 70 75 80

Ile Ala Lys Ile Glu Tyr Ser Thr Asp Phe Pro Val Asn Leu Thr Gly  
 85 90 95

Leu Asp Leu Ser Gln Asn Asn Leu Ser Ser Val Thr Asn Ile Asn Val  
 100 105 110

Lys Lys Met Pro Gln Leu Leu Ser Val Tyr Leu Glu Glu Asn Lys Leu  
 115 120 125

Thr Glu Leu Pro Glu Lys Cys Leu Ser Glu Leu Ser Asn Leu Gln Glu  
 130 135 140

Leu Tyr Ile Asn His Asn Leu Leu Ser Thr Ile Ser Pro Gly Ala Phe  
 145 150 155 160

Ile Gly Leu His Asn Leu Leu Arg Leu His Leu Asn Ser Asn Arg Leu  
 165 170 175

Gln Met Ile Asn Ser Lys Trp Phe Asp Ala Leu Pro Asn Leu Glu Ile  
 180 185 190

Leu Met Ile Gly Glu Asn Pro Ile Ile Arg Ile Lys Asp Met Asn Phe  
 195 200 205

Lys Pro Leu Ile Asn Leu Arg Ser Leu Val Ile Ala Gly Ile Asn Leu  
 210 215 220

Thr Glu Ile Pro Asp Asn Ala Leu Val Gly Leu Glu Asn Leu Glu Ser  
 225 230 235 240

Ile Ser Phe Tyr Asp Asn Arg Leu Ile Lys Val Pro His Val Ala Leu  
 245 250 255

Gln Lys Val Val Asn Leu Lys Phe Leu Asp Leu Asn Lys Asn Pro Ile  
 260 265 270

Asn Arg Ile Arg Arg Gly Asp Phe Ser Asn Met Leu His Leu Lys Glu  
 275 280 285

Leu Gly Ile Asn Asn Met Pro Glu Leu Ile Ser Ile Asp Ser Leu Ala  
 290 295 300

Val Asp Asn Leu Pro Asp Leu Arg Lys Ile Glu Ala Thr Asn Asn Pro  
 305 310 315 320

Arg Leu Ser Tyr Ile His Pro Asn Ala Phe Phe Arg Leu Pro Lys Leu  
 325 330 335

Glu Ser Leu Met Leu Asn Ser Asn Ala Leu Ser Ala Leu Tyr His Gly

T00720-20020610

340	345	350
Thr Ile Glu Ser Leu Pro Asn Leu Lys Glu Ile Ser Ile His Ser Asn		
355	360	365
Pro Ile Arg Cys Asp Cys Val Ile Arg Trp Met Asn Met Asn Lys Thr		
370	375	380
Asn Ile Arg Phe Met Glu Pro Asp Ser Leu Phe Cys Val Asp Pro Pro		
385	390	395
Glu Phe Gln Gly Gln Asn Val Arg Gln Val His Phe Arg Asp Met Met		
405	410	415
Glu Ile Cys Leu Pro Leu Ile Ala Pro Glu Ser Phe Pro Ser Asn Leu		
420	425	430
Asn Val Glu Ala Gly Ser Tyr Val Ser Phe His Cys Arg Ala Thr Ala		
435	440	445
Glu Pro Gln Pro Glu Ile Tyr Trp Ile Thr Pro Ser Gly Gln Lys Leu		
450	455	460
Leu Pro Asn Thr Leu Thr Asp Lys Phe Tyr Val His Ser Glu Gly Thr		
465	470	475
Leu Asp Ile Asn Gly Val Thr Pro Lys Glu Gly Gly Leu Tyr Thr Cys		
485	490	495
Ile Ala Thr Asn Leu Val Gly Ala Asp Leu Lys Ser Val Met Ile Lys		
500	505	510
Val Asp Gly Ser Phe Pro Gln Asp Asn Asn Gly Ser Leu Asn Ile Lys		
515	520	525
Ile Arg Asp Ile Gln Ala Asn Ser Val Leu Val Ser Trp Lys Ala Ser		
530	535	540
Ser Lys Ile Leu Lys Ser Ser Val Lys Trp Thr Ala Phe Val Lys Thr		
545	550	555
Glu Asn Ser His Ala Ala Gln Ser Ala Arg Ile Pro Ser Asp Val Lys		
565	570	575
Val Tyr Asn Leu Thr His Leu Asn Pro Ser Thr Glu Tyr Lys Ile Cys		
580	585	590
Ile Asp Ile Pro Thr Ile Tyr Gln Lys Asn Arg Lys Lys Cys Val Asn		
595	600	605
Val Thr Thr Lys Gly Leu His Pro Asp Gln Lys Glu Tyr Glu Lys Asn		
610	615	620

Thr Asn Met Ser  
705  
  
<210> 70  
<211> 1305  
<212> DNA  
<213> Homo sapiens

<400> 70  
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 ttaccacgt tttggagta gatgaggaat gggctcgta ttatgctgac attccagcat 180  
 gaatctggta gacctgttgt taacccgttc cctctccatg tgtctccctc tacaaaagtt 240  
 ttttttatg atactgtgt ttcatttgc cagatgtgt cccagggt gtcttggc 300  
 ttcccttggg gtttaaatg tcacctgttag caatgcaat ctcaaggaaa tacctagaga 360  
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 tggaaatttt aaggacctcc atcaacttgag agttctcaac ctgtccaaaa atgcattga 480  
 gtttatcgat gagcatgcct tcaaaggagt agctgaaacc ttgcagactc tggacttgc 540  
 cgacaatcggtt attcaaagtg tgcacaaaaa tgccctcaat aacctgaagg ccaggGCCAG 600  
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 gtccaaatcat gagacagccc acaacgtgat ctgtaaaacg tccgtgttgg atgaacatgc 720  
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 taccgattat gcatgtctgg tcaccatgtt tgctgggtt actatggtga tctcatatgt 840  
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 caccccttaa ttgtacccccc gatggatat ttctgagtaa gctactatct gaaacattttg 1200  
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<210> 71  
<211> 259  
<212> PRT  
<213> *Homo sapiens*

<400> 71

Met Asn Leu Val Asp Leu Trp Leu Thr Arg Ser Leu Ser Met Cys Leu  
 1 5 10 15

Leu Leu Gln Ser Phe Val Leu Met Ile Leu Cys Phe His Ser Ala Ser  
 20 25 30

Met Cys Pro Lys Gly Cys Leu Cys Ser Ser Ser Gly Gly Leu Asn Val  
 35 40 45

Thr Cys Ser Asn Ala Asn Leu Lys Glu Ile Pro Arg Asp Leu Pro Pro  
 50 55 60

Glu Thr Val Leu Leu Tyr Leu Asp Ser Asn Gln Ile Thr Ser Ile Pro  
 65 70 75 80

Asn Glu Ile Phe Lys Asp Leu His Gln Leu Arg Val Leu Asn Leu Ser  
 85 90 95

Lys Asn Gly Ile Glu Phe Ile Asp Glu His Ala Phe Lys Gly Val Ala  
 100 105 110

Glu Thr Leu Gln Thr Leu Asp Leu Ser Asp Asn Arg Ile Gln Ser Val  
 115 120 125

His Lys Asn Ala Phe Asn Asn Leu Lys Ala Arg Ala Arg Ile Ala Asn  
 130 135 140

Asn Pro Trp His Cys Asp Cys Thr Leu Gln Gln Val Leu Arg Ser Met  
 145 150 155 160

Ala Ser Asn His Glu Thr Ala His Asn Val Ile Cys Lys Thr Ser Val  
 165 170 175

Leu Asp Glu His Ala Gly Arg Pro Phe Leu Asn Ala Ala Asn Asp Ala  
 180 185 190

Asp Leu Cys Asn Leu Pro Lys Lys Thr Thr Asp Tyr Ala Met Leu Val  
 195 200 205

Thr Met Phe Gly Trp Phe Thr Met Val Ile Ser Tyr Val Val Tyr Tyr  
 210 215 220

Val Arg Gln Asn Gln Glu Asp Ala Arg Arg His Leu Glu Tyr Leu Lys  
 225 230 235 240

Ser Leu Pro Ser Arg Gln Lys Lys Ala Asp Glu Pro Asp Asp Ile Ser  
 245 250 255

Thr Val Val

<210> 72  
 <211> 2290

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 72

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&lt;210&gt; 73

&lt;211&gt; 620

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 73

Met Gln Val Ser Lys Arg Met Leu Ala Gly Gly Val Arg Ser Met Pro

1

5

10

15

TGTGCGCTTCATCAGCCCAAC

Ser Pro Leu Leu Ala Cys Trp Gln Pro Ile Leu Leu Leu Val Leu Gly  
 20                    25                    30

Ser Val Leu Ser Gly Ser Ala Thr Gly Cys Pro Pro Arg Cys Glu Cys  
 35                    40                    45

Ser Ala Gln Asp Arg Ala Val Leu Cys His Arg Lys Cys Phe Val Ala  
 50                    55                    60

Val Pro Glu Gly Ile Pro Thr Glu Thr Arg Leu Leu Asp Leu Gly Lys  
 65                    70                    75                    80

Asn Arg Ile Lys Thr Leu Asn Gln Asp Glu Phe Ala Ser Phe Pro His  
 85                    90                    95

Leu Glu Glu Leu Glu Leu Asn Glu Asn Ile Val Ser Ala Val Glu Pro  
 100                  105                  110

Gly Ala Phe Asn Asn Leu Phe Asn Leu Arg Thr Leu Gly Leu Arg Ser  
 115                  120                  125

Asn Arg Leu Lys Leu Ile Pro Leu Gly Val Phe Thr Gly Leu Ser Asn  
 130                  135                  140

Leu Thr Lys Gln Asp Ile Ser Glu Asn Lys Ile Val Ile Leu Leu Asp  
 145                  150                  155                  160

Tyr Met Phe Gln Asp Leu Tyr Asn Leu Lys Ser Leu Glu Val Gly Asp  
 165                  170                  175

Asn Asp Leu Val Tyr Ile Ser His Arg Ala Phe Ser Gly Leu Asn Ser  
 180                  185                  190

Leu Glu Gln Leu Thr Leu Glu Lys Cys Asn Leu Thr Ser Ile Pro Thr  
 195                  200                  205

Glu Ala Leu Ser His Leu His Gly Leu Ile Val Leu Arg Leu Arg His  
 210                  215                  220

Leu Asn Ile Asn Ala Ile Arg Asp Tyr Ser Phe Lys Arg Leu Tyr Arg  
 225                  230                  235                  240

Leu Lys Val Leu Glu Ile Ser His Trp Pro Tyr Leu Asp Thr Met Thr  
 245                  250                  255

Pro Asn Cys Leu Tyr Gly Leu Asn Leu Thr Ser Leu Ser Ile Thr His  
 260                  265                  270

Cys Asn Leu Thr Ala Val Pro Tyr Leu Ala Val Arg His Leu Val Tyr  
 275                  280                  285

Leu Arg Phe Leu Asn Leu Ser Tyr Asn Pro Ile Ser Thr Ile Glu Gly  
 290                  295                  300

Ser Met Leu His Glu Leu Leu Arg Leu Gln Glu Ile Gln Leu Val Gly  
 305 310 315 320

Gly Gln Leu Ala Val Val Glu Pro Tyr Ala Phe Arg Gly Leu Asn Tyr  
 325 330 335

Leu Arg Val Leu Asn Val Ser Gly Asn Gln Leu Thr Thr Leu Glu Glu  
 340 345 350

Ser Val Phe His Ser Val Gly Asn Leu Glu Thr Leu Ile Leu Asp Ser  
 355 360 365

Asn Pro Leu Ala Cys Asp Cys Arg Leu Leu Trp Val Phe Arg Arg Arg  
 370 375 380

Trp Arg Leu Asn Phe Asn Arg Gln Gln Pro Thr Cys Ala Thr Pro Glu  
 385 390 395 400

Phe Val Gln Gly Lys Glu Phe Lys Asp Phe Pro Asp Val Leu Leu Pro  
 405 410 415

Asn Tyr Phe Thr Cys Arg Arg Ala Arg Ile Arg Asp Arg Lys Ala Gln  
 420 425 430

Gln Val Phe Val Asp Glu Gly His Thr Val Gln Phe Val Cys Arg Ala  
 435 440 445

Asp Gly Asp Pro Pro Ala Ile Leu Trp Leu Ser Pro Arg Lys His  
 450 455 460

Leu Val Ser Ala Lys Ser Asn Gly Arg Leu Thr Val Phe Pro Asp Gly  
 465 470 475 480

Thr Leu Glu Val Arg Tyr Ala Gln Val Gln Asp Asn Gly Thr Tyr Leu  
 485 490 495

Cys Ile Ala Ala Asn Ala Gly Gly Asn Asp Ser Met Pro Ala His Leu  
 500 505 510

His Val Arg Ser Tyr Ser Pro Asp Trp Pro His Gln Pro Asn Lys Thr  
 515 520 525

Phe Ala Phe Ile Ser Asn Gln Pro Gly Glu Gly Glu Ala Asn Ser Thr  
 530 535 540

Arg Ala Thr Val Pro Phe Pro Phe Asp Ile Lys Thr Leu Ile Ile Ala  
 545 550 555 560

Thr Thr Met Gly Phe Ile Ser Phe Leu Gly Val Val Leu Phe Cys Leu  
 565 570 575

Val Leu Leu Phe Leu Trp Ser Arg Gly Lys Gly Asn Thr Lys His Asn

580	585	590
Ile Glu Ile Glu Tyr Val Pro Arg Lys Ser Asp Ala Gly Ile Ser Ser		
595	600	605

Ala Asp Ala Pro Arg Lys Phe Asn Met Lys Met Ile		
610	615	620

<210> 74  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 74		22
tcacacctggag cctttattgg cc		

<210> 75  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 75		23
ataccagcta taaccaggct gcg		

<210> 76  
<211> 52  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 76		50
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gg		52

<210> 77  
<211> 22  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

DRAFT DRAFT DRAFT

<400> 77 ccatgtgtct cctcctacaa ag	22
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<210> 79 <211> 50 <212> DNA <213> Artificial Sequence	
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<210> 80 <211> 22 <212> DNA <213> Artificial Sequence	
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<400> 80 agcaaccgcc tgaagctcat cc	22
<210> 81 <211> 24 <212> DNA <213> Artificial Sequence	
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<400> 81 aaggcgcggt gaaagatgta gacg	24
<210> 82	



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 Pro Trp Thr Ser Asp Glu Thr Val Val Ala Gly Gly Thr Val Val Leu  
 35 40 45  
 Lys Cys Gln Val Lys Asp His Glu Asp Ser Ser Leu Gln Trp Ser Asn  
 50 55 60  
 Pro Ala Gln Gln Thr Leu Tyr Phe Gly Glu Lys Arg Ala Leu Arg Asp  
 65 70 75 80  
 Asn Arg Ile Gln Leu Val Thr Ser Thr Pro His Glu Leu Ser Ile Ser  
 85 90 95  
 Ile Ser Asn Val Ala Leu Ala Asp Glu Gly Glu Tyr Thr Cys Ser Ile  
 100 105 110  
 Phe Thr Met Pro Val Arg Thr Ala Lys Ser Leu Val Thr Val Leu Gly  
 115 120 125  
 Ile Pro Gln Lys Pro Ile Ile Thr Gly Tyr Lys Ser Ser Leu Arg Glu  
 130 135 140  
 Lys Asp Thr Ala Thr Leu Asn Cys Gln Ser Ser Gly Ser Lys Pro Ala  
 145 150 155 160  
 Ala Arg Leu Thr Trp Arg Lys Gly Asp Gln Glu Leu His Gly Glu Pro  
 165 170 175  
 Thr Arg Ile Gln Glu Asp Pro Asn Gly Lys Thr Phe Thr Val Ser Ser  
 180 185 190  
 Ser Val Thr Phe Gln Val Thr Arg Glu Asp Asp Gly Ala Ser Ile Val  
 195 200 205  
 Cys Ser Val Asn His Glu Ser Leu Lys Gly Ala Asp Arg Ser Thr Ser  
 210 215 220  
 Gln Arg Ile Glu Val Leu Tyr Thr Pro Thr Ala Met Ile Arg Pro Asp  
 225 230 235 240  
 Pro Pro His Pro Arg Glu Gly Gln Lys Leu Leu Leu His Cys Glu Gly  
 245 250 255  
 Arg Gly Asn Pro Val Pro Gln Gln Tyr Leu Trp Glu Lys Glu Gly Ser  
 260 265 270  
 Val Pro Pro Leu Lys Met Thr Gln Glu Ser Ala Leu Ile Phe Pro Phe  
 275 280 285

Leu Asn Lys Ser Asp Ser Gly Thr Tyr Gly Cys Thr Ala Thr Ser Asn  
 290 295 300

Met Gly Ser Tyr Lys Ala Tyr Tyr Thr Leu Asn Val Asn Asp Pro Ser  
 305 310 315 320

Pro Val Pro Ser Ser Ser Thr Tyr His Ala Ile Ile Gly Gly Ile  
 325 330 335

Val Ala Phe Ile Val Phe Leu Leu Leu Ile Met Leu Ile Phe Leu Gly  
 340 345 350

His Tyr Leu Ile Arg His Lys Gly Thr Tyr Leu Thr His Glu Ala Lys  
 355 360 365

Gly Ser Asp Asp Ala Pro Asp Ala Asp Thr Ala Ile Ile Asn Ala Glu  
 370 375 380

Gly Gly Gln Ser Gly Gly Asp Asp Lys Lys Glu Tyr Phe Ile  
 385 390 395

<210> 85

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 85

gcttaggaatt ccacagaagc cc

22

<210> 86

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 86

aacctggaat gtcaccgagc tg

22

<210> 87

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

oligonucleotide probe

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<400> 87
cctagcacag tgacgaggga cttggc 26

<210> 88
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 88
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<210> 89
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 89
gccctggcag acgagggcga gtacacctgc tcaatcttca ctatgcctgt 50

<210> 90
<211> 2755
<212> DNA
<213> Homo sapiens

<400> 90
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gctgttactt tgtatgaga tcggggatga attgctcgct taaaaaatgc tgcttggat 180
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<210> 91

<211> 696

<212> PRT

<213> Homo sapiens

<400> 91

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Glu Ile Glu Gly Asp Leu His Val Asp Cys Glu Lys Lys Gly Phe Thr  
 35 40 45

Ser Leu Gln Arg Phe Thr Ala Pro Thr Ser Gln Phe Tyr His Leu Phe  
 50 55 60

Leu His Gly Asn Ser Leu Thr Arg Leu Phe Pro Asn Glu Phe Ala Asn  
 65 70 75 80

Phe Tyr Asn Ala Val Ser Leu His Met Glu Asn Asn Gly Leu His Glu  
 85 90 95

Ile Val Pro Gly Ala Phe Leu Gly Leu Gln Leu Val Lys Arg Leu His  
 100 105 110

Ile Asn Asn Asn Lys Ile Lys Ser Phe Arg Lys Gln Thr Phe Leu Gly  
 115 120 125

Leu Asp Asp Leu Glu Tyr Leu Gln Ala Asp Phe Asn Leu Leu Arg Asp  
 130 135 140

Ile Asp Pro Gly Ala Phe Gln Asp Leu Asn Lys Leu Glu Val Leu Ile  
 145 150 155 160

Leu Asn Asp Asn Leu Ile Ser Thr Leu Pro Ala Asn Val Phe Gln Tyr  
 165 170 175

Val Pro Ile Thr His Leu Asp Leu Arg Gly Asn Arg Leu Lys Thr Leu  
 180 185 190

Pro Tyr Glu Glu Val Leu Glu Gln Ile Pro Gly Ile Ala Glu Ile Leu  
 195 200 205

Leu Glu Asp Asn Pro Trp Asp Cys Thr Cys Asp Leu Leu Ser Leu Lys  
 210 215 220

Glu Trp Leu Glu Asn Ile Pro Lys Asn Ala Leu Ile Gly Arg Val Val  
 225 230 235 240

Cys Glu Ala Pro Thr Arg Leu Gln Gly Lys Asp Leu Asn Glu Thr Thr  
 245 250 255

Glu Gln Asp Leu Cys Pro Leu Lys Asn Arg Val Asp Ser Ser Leu Pro  
 260 265 270

Ala Pro Pro Ala Gln Glu Glu Thr Phe Ala Pro Gly Pro Leu Pro Thr  
 275 280 285

Pro Phe Lys Thr Asn Gly Gln Glu Asp His Ala Thr Pro Gly Ser Ala  
 290 295 300

Pro Asn Gly Gly Thr Lys Ile Pro Gly Asn Trp Gln Ile Lys Ile Arg  
 305 310 315 320

Pro Thr Ala Ala Ile Ala Thr Gly Ser Ser Arg Asn Lys Pro Leu Ala  
 325 330 335

Asn Ser Leu Pro Cys Pro Gly Gly Cys Ser Cys Asp His Ile Pro Gly  
 340 345 350

Ser Gly Leu Lys Met Asn Cys Asn Asn Arg Asn Val Ser Ser Leu Ala  
 355 360 365

Asp Leu Lys Pro Lys Leu Ser Asn Val Gln Glu Leu Phe Leu Arg Asp  
 370 375 380

Asn Lys Ile His Ser Ile Arg Lys Ser His Phe Val Asp Tyr Lys Asn  
 385 390 395 400  
 Leu Ile Leu Leu Asp Leu Gly Asn Asn Asn Ile Ala Thr Val Glu Asn  
 405 410 415  
 Asn Thr Phe Lys Asn Leu Leu Asp Leu Arg Trp Leu Tyr Met Asp Ser  
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 Gly Thr Phe Asn Ala Met Pro Lys Leu Arg Ile Leu Ile Leu Asn Asn  
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 485 490 495  
 Ser Lys Leu Ser Leu His Asn Asn Tyr Phe Met Tyr Leu Pro Val Ala  
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 Gly Val Leu Asp Gln Leu Thr Ser Ile Ile Gln Ile Asp Leu His Gly  
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 Pro Val Asn Phe Phe Arg Lys Asp Phe Met Leu Leu Ser Asn Asp Glu  
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 Tyr Leu Asp Thr Ser Arg Val Ser Ile Ser Val Leu Val Pro Gly Leu  
 610 615 620  
 Leu Leu Val Phe Val Thr Ser Ala Phe Thr Val Val Gly Met Leu Val  
 625 630 635 640  
 Phe Ile Leu Arg Asn Arg Lys Arg Ser Lys Arg Arg Asp Ala Asn Ser  
 645 650 655  
 Ser Ala Ser Glu Ile Asn Ser Leu Gln Thr Val Cys Asp Ser Ser Tyr

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Cys Gly Ser His Ser Leu Ser Asp		
690	695	
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<212> DNA		
<213> Artificial Sequence		
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<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		
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<210> 93		
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<212> DNA		
<213> Artificial Sequence		
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 gagaacatgg ccaatcaggg tcgacgagaa gctggagag acaccacttg tccctgaaca 1320  
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 aatttacatt aaaaaataat ttctaccaaa atggaaagga aatgttctat gttgttcagg 2160  
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 gttgtat 2226

<210> 96  
 <211> 490  
 <212> PRT  
 <213> Homo sapiens

<400> 96  
 Met Arg Pro Ala Phe Ala Leu Cys Leu Leu Trp Gln Ala Leu Trp Pro  
 1 5 10 15

Gly Pro Gly Gly Glu His Pro Thr Ala Asp Arg Ala Gly Cys Ser  
 20 25 30

Ala Ser Gly Ala Cys Tyr Ser Leu His His Ala Thr Met Lys Arg Gln  
 35 40 45

Ala Ala Glu Glu Ala Cys Ile Leu Arg Gly Gly Ala Leu Ser Thr Val  
 50 55 60

Arg Ala Gly Ala Glu Leu Arg Ala Val Leu Ala Leu Leu Arg Ala Gly  
 65 70 75 80

Pro Gly Pro Gly Gly Ser Lys Asp Leu Leu Phe Trp Val Ala Leu  
 85 90 95

Glu Arg Arg Arg Ser His Cys Thr Leu Glu Asn Glu Pro Leu Arg Gly  
 100 105 110

Phe Ser Trp Leu Ser Ser Asp Pro Gly Gly Leu Glu Ser Asp Thr Leu  
 115 120 125

Gln Trp Val Glu Glu Pro Gln Arg Ser Cys Thr Ala Arg Arg Cys Ala  
 130 135 140

Val Leu Gln Ala Thr Gly Gly Val Glu Pro Ala Gly Trp Lys Glu Met  
 145 150 155 160

Arg Cys His Leu Arg Ala Asn Gly Tyr Leu Cys Lys Tyr Gln Phe Glu  
 165 170 175

Val Leu Cys Pro Ala Pro Arg Pro Gly Ala Ala Ser Asn Leu Ser Tyr  
 180 185 190

Arg Ala Pro Phe Gln Leu His Ser Ala Ala Leu Asp Phe Ser Pro Pro  
 195 200 205

Gly Thr Glu Val Ser Ala Leu Cys Arg Gly Gln Leu Pro Ile Ser Val  
 210 215 220

Thr Cys Ile Ala Asp Glu Ile Gly Ala Arg Trp Asp Lys Leu Ser Gly  
 225 230 235 240

Asp Val Leu Cys Pro Cys Pro Gly Arg Tyr Leu Arg Ala Gly Lys Cys  
 245 250 255

Ala Glu Leu Pro Asn Cys Leu Asp Asp Leu Gly Gly Phe Ala Cys Glu  
 260 265 270

Cys Ala Thr Gly Phe Glu Leu Gly Lys Asp Gly Arg Ser Cys Val Thr  
 275 280 285

Ser Gly Glu Gly Gln Pro Thr Leu Gly Gly Thr Gly Val Pro Thr Arg  
 290 295 300

Arg Pro Pro Ala Thr Ala Thr Ser Pro Val Pro Gln Arg Thr Trp Pro  
 305 310 315 320

Ile Arg Val Asp Glu Lys Leu Gly Glu Thr Pro Leu Val Pro Glu Gln  
 325 330 335

Asp Asn Ser Val Thr Ser Ile Pro Glu Ile Pro Arg Trp Gly Ser Gln

340	345	350
Ser Thr Met Ser Thr Leu Gln Met Ser Leu Gln Ala Glu Ser Lys Ala		
355	360	365
Thr Ile Thr Pro Ser Gly Ser Val Ile Ser Lys Phe Asn Ser Thr Thr		
370	375	380
Ser Ser Ala Thr Pro Gln Ala Phe Asp Ser Ser Ser Ala Val Val Phe		
385	390	395
Ile Phe Val Ser Thr Ala Val Val Val Leu Val Ile Leu Thr Met Thr		
405	410	415
Val Leu Gly Leu Val Lys Leu Cys Phe His Glu Ser Pro Ser Ser Gln		
420	425	430
Pro Arg Lys Glu Ser Met Gly Pro Pro Gly Leu Glu Ser Asp Pro Glu		
435	440	445
Pro Ala Ala Leu Gly Ser Ser Ser Ala His Cys Thr Asn Asn Gly Val		
450	455	460
Lys Val Gly Asp Cys Asp Leu Arg Asp Arg Ala Glu Gly Ala Leu Leu		
465	470	475
Ala Glu Ser Pro Leu Gly Ser Ser Asp Ala		
485	490	

&lt;210&gt; 97

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 97

tggaaggaga tgcgatgcc a cctg

24

&lt;210&gt; 98

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 98

tgaccagtgg ggaaggacag

20

<210> 99  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 99  
acagagcaga ggggccttg 20

<210> 100  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 100  
tcagggacaa gtgggtctc tccc 24

<210> 101  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 101  
tcagggagg agtgtgcagt tctg 24

<210> 102  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 102  
acagccccg atctcaggta cttgcattcg gc ggacgaaatc ggcgctcgct 50

<210> 103  
<211> 2026  
<212> DNA  
<213> Homo sapiens

<400> 103

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 tatccccgg ctacctggc cgccccgcgg cggtgcgcg gtgagaggga gcgcgcggc 180  
 agccgagcgc cggtgtgagc cagcgctgct gccagtgtga gcccgggtgt gagcgcggc 240  
 ggtgcggagg ggcgtgtgt ccggcgcgcg cgccgtggg tgcaaacccc gagcgtctac 300  
 gctccatga ggggcgcgaa cgctggcgc ccactctgcc tgctgctggc tgccgccacc 360  
 cagctctcgcc ggcagcagtc cccagagaga cctgtttca catgtggtgg cattcttact 420  
 ggagagtctg gatttattgg cagtgaaggt tttcctggag tgtaccctcc aaatagcaaa 480  
 tgtacttgaa aaatcacagt tccccaagga aaagtagtgc ttctcaattt ccgattcata 540  
 gacctcgaga gtgacaacct gtggcgttat gactttgtgg atgtgtacaa tggccatgcc 600  
 aatggccagc gcattggccg ctctgtggc actttccggc ctggagccct tgcgtccagt 660  
 ggcacaacaaga tgcgtgtca gatgatttct gatgccaaca cagctggcaa tggcttcatg 720  
 gccatgttct ccgctgtga accaaacgaa agaggggatc agatattgtgg aggactcctt 780  
 gacagacccctt ccggcttttaaaaacccccc aactggccag accgggatta ccctgcagga 840  
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 ctaaaagtgttgcgacggg cagcttggaa gcgtttatattt atacatctctt gtaaaaggat 1860  
 attttagaat tgagttgtgt gaagatgtca aaaaaagatt tttagaagtgc aatattata 1920  
 gtgttatttgcgttacaccccttgc aaggcatttgc cctgagggtgt tacaatcttgcgtt 1980  
 tctaaatcaa tgcttaataaaatatttttaaaggaaaaaaa aaaaaaa 2026

&lt;210&gt; 104

&lt;211&gt; 415

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 104

Met	Arg	Gly	Ala	Asn	Ala	Trp	Ala	Pro	Leu	Cys	Leu	Leu	Leu	Ala	Ala
1															15

Ala	Thr	Gln	Leu	Ser	Arg	Gln	Gln	Ser	Pro	Glu	Arg	Pro	Val	Phe	Thr
															30
20															

Cys	Gly	Gly	Ile	Leu	Thr	Gly	Glu	Ser	Gly	Phe	Ile	Gly	Ser	Glu	Gly
															45
35															

Phe	Pro	Gly	Val	Tyr	Pro	Pro	Asn	Ser	Lys	Cys	Thr	Trp	Lys	Ile	Thr
															50
															55
															60

Val Pro Glu Gly Lys Val Val Val Leu Asn Phe Arg Phe Ile Asp Leu  
 65 70 75 80

Glu Ser Asp Asn Leu Cys Arg Tyr Asp Phe Val Asp Val Tyr Asn Gly  
 85 90 95

His Ala Asn Gly Gln Arg Ile Gly Arg Phe Cys Gly Thr Phe Arg Pro  
 100 105 110

Gly Ala Leu Val Ser Ser Gly Asn Lys Met Met Val Gln Met Ile Ser  
 115 120 125

Asp Ala Asn Thr Ala Gly Asn Gly Phe Met Ala Met Phe Ser Ala Ala  
 130 135 140

Glu Pro Asn Glu Arg Gly Asp Gln Tyr Cys Gly Gly Leu Leu Asp Arg  
 145 150 155 160

Pro Ser Gly Ser Phe Lys Thr Pro Asn Trp Pro Asp Arg Asp Tyr Pro  
 165 170 175

Ala Gly Val Thr Cys Val Trp His Ile Val Ala Pro Lys Asn Gln Leu  
 180 185 190

Ile Glu Leu Lys Phe Glu Lys Phe Asp Val Glu Arg Asp Asn Tyr Cys  
 195 200 205

Arg Tyr Asp Tyr Val Ala Val Phe Asn Gly Gly Glu Val Asn Asp Ala  
 210 215 220

Arg Arg Ile Gly Lys Tyr Cys Gly Asp Ser Pro Pro Ala Pro Ile Val  
 225 230 235 240

Ser Glu Arg Asn Glu Leu Leu Ile Gln Phe Leu Ser Asp Leu Ser Leu  
 245 250 255

Thr Ala Asp Gly Phe Ile Gly His Tyr Ile Phe Arg Pro Lys Lys Leu  
 260 265 270

Pro Thr Thr Thr Glu Gln Pro Val Thr Thr Phe Pro Val Thr Thr  
 275 280 285

Gly Leu Lys Pro Thr Val Ala Leu Cys Gln Gln Lys Cys Arg Arg Thr  
 290 295 300

Gly Thr Leu Glu Gly Asn Tyr Cys Ser Ser Asp Phe Val Leu Ala Gly  
 305 310 315 320

Thr Val Ile Thr Thr Ile Thr Arg Asp Gly Ser Leu His Ala Thr Val  
 325 330 335

Ser Ile Ile Asn Ile Tyr Lys Glu Gly Asn Leu Ala Ile Gln Gln Ala

340	345	350
Gly Lys Asn Met Ser Ala Arg Leu Thr Val Val Cys Lys Gln Cys Pro		
355	360	365

Leu Leu Arg Arg Gly Leu Asn Tyr Ile Ile Met Gly Gln Val Gly Glu		
370	375	380

Asp Gly Arg Gly Lys Ile Met Pro Asn Ser Phe Ile Met Met Phe Lys			
385	390	395	400

Thr Lys Asn Gln Lys Leu Leu Asp Ala Leu Lys Asn Lys Gln Cys		
405	410	415

<210> 105

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 105

ccgattcata gacctcgaga gt

22

<210> 106

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 106

gtcaaggagt cctccacaat ac

22

<210> 107

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 107

gtgtacaatg gccatgccaa tggccagcgc attggccgct tctgt

45

<210> 108

<211> 1838

<212> DNA

<213> Homo sapiens

<400> 108

cggacgcgtg ggcggacgcg tggcgcccc acggcgcggc cgggctgggg cggtcgcttc 60  
 ttcccttcac gttggctacg agggtccccca gcctggtaa agatggcccc atggccccc 120  
 aagggcctag tcccaagctgt gctctgggc ctcagcctct tcctcaaacct cccaggac 180  
 atctggctcc agccctctcc acctccccag ttttctcccc cgcctcagcc ccatccgtgt 240  
 catacctgcc ggggacttgt tgacagctt aacaaggggcc tggagagaac catccggac 300  
 aactttggag gtggaaacac tgcctggag gaagagaatt tgtccaaata caaagacagt 360  
 gagaccgcgc tggtagaggt gctggagggt gtgtgcagca agtcagactt cgagtgcac 420  
 cgcctgcgtt agctgagtga ggagctgggt gagagctggg gtttcacaa gcagcaggag 480  
 gccccggacc tcttccagtg gctgtgctca gatcccctga agctctgctg ccccgccaggc 540  
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 tacgggggtg aggcctgtgg ccagtgtggc cttggctact ttgaggcaga acgcaacgccc 720  
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 tcaaaactgtt tgcaatgcaa gaagggtctt gcccgtcattt acctcaagtg tgttagacatt 840  
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 ggctcctatg agtgcgcgaga ctgtgccaag gcctgcctag gctgcattttt ggcaggggcca 960  
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 gatgagtgta agacagaggt gtgtccggga gagaacaaggc agtgtgaaaaa caccggggc 1080  
 gtttatcgct gcatctgtgc cgagggtctac aagcagatgg aaggcatctg tgtgaaggag 1140  
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 gataccatga gcttttcacc tggcggggac tggcaggctt cacaatgtgt gaatttcaaa 1620  
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 acaggggtgg ggccatcaca gtccttcctt gccagctgca tgctgccagt tcctgttctg 1740  
 tgttcaccac atccccacac cccattgcca cttattttt catctcaggaa aataaaagaaa 1800  
 ggtcttgaa agttaaaaaa aaaaaaaaaa aaaaaaaaaa 1838

<210> 109

<211> 420

<212> PRT

<213> Homo sapiens

<400> 109

Met Ala Pro Trp Pro Pro Lys Gly Leu Val Pro Ala Val Leu Trp Gly  
1 5 10 15

Leu Ser Leu Phe Leu Asn Leu Pro Gly Pro Ile Trp Leu Gln Pro Ser  
 20 25 30

Pro Pro Pro Gln Ser Ser Pro Pro Pro Gln Pro His Pro Cys His Thr  
35 40 45

Cys Arg Gly Leu Val Asp Ser Phe Asn Lys Gly Leu Glu Arg Thr Ile  
 50 55 60

Arg Asp Asn Phe Gly Gly Asn Thr Ala Trp Glu Glu Glu Asn Leu  
 65 70 75 80

Ser Lys Tyr Lys Asp Ser Glu Thr Arg Leu Val Glu Val Leu Glu Gly  
 85 90 95

Val Cys Ser Lys Ser Asp Phe Glu Cys His Arg Leu Leu Glu Leu Ser  
 100 105 110

Glu Glu Leu Val Glu Ser Trp Trp Phe His Lys Gln Gln Glu Ala Pro  
 115 120 125

Asp Leu Phe Gln Trp Leu Cys Ser Asp Ser Leu Lys Leu Cys Cys Pro  
 130 135 140

Ala Gly Thr Phe Gly Pro Ser Cys Leu Pro Cys Pro Gly Gly Thr Glu  
 145 150 155 160

Arg Pro Cys Gly Gly Tyr Gly Gln Cys Glu Gly Glu Gly Thr Arg Gly  
 165 170 175

Gly Ser Gly His Cys Asp Cys Gln Ala Gly Tyr Gly Gly Glu Ala Cys  
 180 185 190

Gly Gln Cys Gly Leu Gly Tyr Phe Glu Ala Glu Arg Asn Ala Ser His  
 195 200 205

Leu Val Cys Ser Ala Cys Phe Gly Pro Cys Ala Arg Cys Ser Gly Pro  
 210 215 220

Glu Glu Ser Asn Cys Leu Gln Cys Lys Lys Gly Trp Ala Leu His His  
 225 230 235 240

Leu Lys Cys Val Asp Ile Asp Glu Cys Gly Thr Glu Gly Ala Asn Cys  
 245 250 255

Gly Ala Asp Gln Phe Cys Val Asn Thr Glu Gly Ser Tyr Glu Cys Arg  
 260 265 270

Asp Cys Ala Lys Ala Cys Leu Gly Cys Met Gly Ala Gly Pro Gly Arg  
 275 280 285

Cys Lys Lys Cys Ser Pro Gly Tyr Gln Gln Val Gly Ser Lys Cys Leu  
 290 295 300

Asp Val Asp Glu Cys Glu Thr Glu Val Cys Pro Gly Glu Asn Lys Gln  
 305 310 315 320

Cys Glu Asn Thr Glu Gly Gly Tyr Arg Cys Ile Cys Ala Glu Gly Tyr  
 325 330 335

Lys Gln Met Glu Gly Ile Cys Val Lys Glu Gln Ile Pro Glu Ser Ala  
 340 345 350

Gly Phe Phe Ser Glu Met Thr Glu Asp Glu Leu Val Val Leu Gln Gln  
 355 360 365

Met Phe Phe Gly Ile Ile Ile Cys Ala Leu Ala Thr Leu Ala Ala Lys  
 370 375 380

Gly Asp Leu Val Phe Thr Ala Ile Phe Ile Gly Ala Val Ala Ala Met  
 385 390 395 400

Thr Gly Tyr Trp Leu Ser Glu Arg Ser Asp Arg Val Leu Glu Gly Phe  
 405 410 415

Ile Lys Gly Arg  
 420

<210> 110

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 110

cctggctatc agcaggtggg ctccaaagtgt ctcgatgtgg atgagtgtga 50

<210> 111

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 111

attctgcgtg aacactgagg gc 22

<210> 112

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 112

atctgcttgt agccctcgcc ac 22

<210> 113

&lt;211&gt; 1616

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; modified\_base

&lt;222&gt; (1461)

&lt;223&gt; a, t, c or g

&lt;400&gt; 113

tgagaccctc ctgcagccctt ctcaaggac agccccactc tgccctttgc tcctccaggg 60  
 cagcaccatg cagccccgtg ggctctgtcg ggcactctgg gtgttgccccc tggccagccc 120  
 cggggccgccc ctgaccgggg agcagctctt gggcagccctg ctgcggcagc tgcaactcaa 180  
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 gcccagtac gtggccctgc tgcaagcgcag ccacggggac cgctcccgcg gaaagagggtt 300  
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 gctgggttgc ggcattggagc agccggctgcc gccaacacgc gagctgggtgc aggccgtgt 420  
 gcggtcttc caggagccgg tcccaaggc cgccgtgcac aggcacgggc ggctgtcccc 480  
 ggcacgcgc cggggccggg tgaccgtcgat gtggctgcgc gtccgcgcac acggctccaa 540  
 cccacactcc ctcatcgact ccaggctgggt gtccgtccac gagagcggct ggaaggcctt 600  
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 gtcacaggtg tcgggtcgaga gggagcatct gggcccgctg gctccggcg cccacaagct 720  
 ggtccgctt gcctcgccagg gggccgcaccc cgggcttggg gagccccagc tggagctgca 780  
 caccctggac cttggggact atggagctca gggcgactgt gaccctgaag caccaatgac 840  
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 cgagaactgg gtgtggagc ccccggttt cctggcttat gagtgtgtgg gcacctgccc 960  
 gcagcccccg gaggccctgg cttcaagtg gccgttctg ggcctcgac agtgcac 1020  
 ctcggagact gactcgctgc ccatgatcgat cagcatcaag gagggaggca ggaccaggcc 1080  
 ccaggtggtc agcctgcca acatgagggt gcaagatgc agctgtgcct cggatgggtgc 1140  
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 gtgtgtgttt ctgaagtgtt cgagggtacc agagagctg gcatgtactg aactgtgtat 1260  
 ggacaaatgc tctgtgtct cttagtggacc ctgaatttgc ttccctctgac aagttacctc 1320  
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 aaagtccctcc accaccactc tggacctaag acctgggtt aagtgtgggt tgtgcacccc 1560  
 caatccagat aataaagact ttgtaaaaca tgaataaaac acattttattt ctaaaa 1616

&lt;210&gt; 114

&lt;211&gt; 366

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 114

Met Gln Pro Leu Trp Leu Cys Trp Ala Leu Trp Val Leu Pro Leu Ala

1

5

10

15

Ser Pro Gly Ala Ala Leu Thr Gly Glu Gln Leu Leu Gly Ser Leu Leu

20

25

30

Arg Gln Leu Gln Leu Lys Glu Val Pro Thr Leu Asp Arg Ala Asp Met

35

40

45

Glu Glu Leu Val Ile Pro Thr His Val Arg Ala Gln Tyr Val Ala Leu  
 50 55 60

Leu Gln Arg Ser His Gly Asp Arg Ser Arg Gly Lys Arg Phe Ser Gln  
 65 70 75 80

Ser Phe Arg Glu Val Ala Gly Arg Phe Leu Ala Leu Glu Ala Ser Thr  
 85 90 95

His Leu Leu Val Phe Gly Met Glu Gln Arg Leu Pro Pro Asn Ser Glu  
 100 105 110

Leu Val Gln Ala Val Leu Arg Leu Phe Gln Glu Pro Val Pro Lys Ala  
 115 120 125

Ala Leu His Arg His Gly Arg Leu Ser Pro Arg Ser Ala Arg Ala Arg  
 130 135 140

Val Thr Val Glu Trp Leu Arg Val Arg Asp Asp Gly Ser Asn Arg Thr  
 145 150 155 160

Ser Leu Ile Asp Ser Arg Leu Val Ser Val His Glu Ser Gly Trp Lys  
 165 170 175

Ala Phe Asp Val Thr Glu Ala Val Asn Phe Trp Gln Gln Leu Ser Arg  
 180 185 190

Pro Arg Gln Pro Leu Leu Gln Val Ser Val Gln Arg Glu His Leu  
 195 200 205

Gly Pro Leu Ala Ser Gly Ala His Lys Leu Val Arg Phe Ala Ser Gln  
 210 215 220

Gly Ala Pro Ala Gly Leu Gly Glu Pro Gln Leu Glu Leu His Thr Leu  
 225 230 235 240

Asp Leu Gly Asp Tyr Gly Ala Gln Gly Asp Cys Asp Pro Glu Ala Pro  
 245 250 255

Met Thr Glu Gly Thr Arg Cys Cys Arg Gln Glu Met Tyr Ile Asp Leu  
 260 265 270

Gln Gly Met Lys Trp Ala Glu Asn Trp Val Leu Glu Pro Pro Gly Phe  
 275 280 285

Leu Ala Tyr Glu Cys Val Gly Thr Cys Arg Gln Pro Pro Glu Ala Leu  
 290 295 300

Ala Phe Lys Trp Pro Phe Leu Gly Pro Arg Gln Cys Ile Ala Ser Glu  
 305 310 315 320

Thr Asp Ser Leu Pro Met Ile Val Ser Ile Lys Glu Gly Gly Arg Thr  
 325 330 335

Arg Pro Gln Val Val Ser Leu Pro Asn Met Arg Val Gln Lys Cys Ser  
 340 345 350

Cys Ala Ser Asp Gly Ala Leu Val Pro Arg Arg Leu Gln Pro  
 355 360 365

<210> 115

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 115

aggactgccat aacttgcct g

21

<210> 116

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 116

ataggagttg aagcagcgct gc

22

<210> 117

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 117

tgtgtggaca tagacgagtgc cgcttaccgc tactgccagc accgc

45

<210> 118

<211> 1857

<212> DNA

<213> Homo sapiens

<400> 118

gtctgttccc aggagtccctt cggcggtgtgt gctgtcactg gctgtatcgat gatggggaca 60  
 aaggcgcaag tcgagagaa actgttgtgc ctcttcataat tgccatcct gttgtgtcc 120  
 ctggcattgg gcaatgttac agtgcactt tctgaacctg aagtcaaat ttctgagaat 180

aatcctgtga agttgtcctg tgccactcg ggctttctt ctcgggtgt ggagtggaaag 240  
 tttgaccaag gagacaccac cagactcggt tgctataata acaagatcac agttcctat 300  
 gaggaccggg tgaccttctt gcacaactgggt atcacctca agtccgtgac acggaaagac 360  
 actggacat acacttgat ggtctctgag gaaggcggca acagctatgg ggaggtcaag 420  
 gtcaagctca tcgtgcttgt gcctccatcc aagcctacag ttaacatccc ctctctgcc 480  
 accattggga accgggcagt gctgacatgc tcagaacaag atggttcccc accttctgaa 540  
 tacacctggt tcaaagatgg gatagtatg cctacgaatc cccaaagcac ccgtgccttc 600  
 agcaactt cctatgtcct gaatcccaca acaggagagc tggctttga tcccctgtca 660  
 gcctctgata ctggagaata cagctgtgag gcacggaatg ggtatggac acccatgact 720  
 tcaaattctg tgccatcgga agctgtggag cggaaatgtgg gggtcatcggt ggcagccgtc 780  
 cttgtAACCC tgattctcctt gggaaatctt gttttggca tctggtttgc ctatagccga 840  
 ggccactttg acagaacaaa gaaaggact tcgagtaaga agtgcattt cagccagcct 900  
 agtgcggaa gtgaaggaga attcaaacag acctcgcat tcctgggtgt agcctggcg 960  
 gctcaccggcc tatcatctgc atttgccta ctcagggtct accggactct ggccctgtat 1020  
 gtctgttagtt tcacaggatg ctttacacc cccacaggcc ccctacttct 1080  
 tcggatgtgt tttaataat gtcagctatg tgcccatcc tcctcatgc cctccctccc 1140  
 tttcttacca ctgctgagtg gcctggaaact tgtttaaagt gtttattccc cattttttg 1200  
 agggatcagg aaggaatctt gggatggcca ttgacttccc ttctaaatggtag acagcaaaaa 1260  
 tggccgggggt cgccggaaatc tgcaactcaac tgcccacctg gctggcaggg atcttgaat 1320  
 aggtatctt agcttgggtc tggctctt ctttgcgtac tgacgaccag ggccagctgt 1380  
 tctagagcgg gaatttagagg ctagagcggc tgaaatgggtt gtttgggtat gacactgggg 1440  
 tcctccatc tctggggggcc actctttctt gtcttccat gggaaatgtcc actggatcc 1500  
 ctctggccctg tcctcctgaa tacaagctga ctgacattga ctgtgtctgt ggaaaatggg 1560  
 agctttgtt gtggagagca tagtaaattt tcagagaact tgaagccaaa aggattaaa 1620  
 accgctgtc taaagaaaag aaaactggag gctggccgcgca gtggctcacg cctgtaatcc 1680  
 cagaggctga ggcaggccgaa tcacctgagg tcgggagttc gggatcagcc tgaccaacat 1740  
 ggagaaaccc tactggaaat acaaagttt ccaggcatgg tgggtgcattc ctgttagtccc 1800  
 agtgcgtcag gagcctggca acaagagcaa aactccagct caaaaaaaaaaaaaaaa 1857

&lt;210&gt; 119

&lt;211&gt; 299

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 119

Met	Gly	Thr	Lys	Ala	Gln	Val	Glu	Arg	Lys	Leu	Leu	Cys	Leu	Phe	Ile
1															

5

10

15

Leu	Ala	Ile	Leu	Leu	Cys	Ser	Leu	Ala	Leu	Gly	Ser	Val	Thr	Val	His
20															

25

30

Ser	Ser	Glu	Pro	Glu	Val	Arg	Ile	Pro	Glu	Asn	Asn	Pro	Val	Lys	Leu
35															

40

45

Ser	Cys	Ala	Tyr	Ser	Gly	Phe	Ser	Ser	Pro	Arg	Val	Glu	Trp	Lys	Phe
50															

55

60

Asp	Gln	Gly	Asp	Thr	Thr	Arg	Leu	Val	Cys	Tyr	Asn	Asn	Lys	Ile	Thr
65															

70

75

80

Ala	Ser	Tyr	Glu	Asp	Arg	Val	Thr	Phe	Leu	Pro	Thr	Gly	Ile	Thr	Phe
85															

90

95

Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser  
 100 105 110

Glu Glu Gly Gly Asn Ser Tyr Gly Glu Val Lys Val Lys Leu Ile Val  
 115 120 125

Leu Val Pro Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr  
 130 135 140

Ile Gly Asn Arg Ala Val Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro  
 145 150 155 160

Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn  
 165 170 175

Pro Lys Ser Thr Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro  
 180 185 190

Thr Thr Gly Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly  
 195 200 205

Glu Tyr Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser  
 210 215 220

Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val  
 225 230 235 240

Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Ile Leu Val Phe Gly  
 245 250 255

Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys Lys Gly  
 260 265 270

Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser Glu  
 275 280 285

Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val  
 290 295

<210> 120

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 120

tcggcgagct gtgttctgtt tccc

24

<210> 121

<211> 50

FOURTY EIGHT

```
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 121
tgatcgcgat ggggacaaaag gcgcaagctc gagagggaaac ttttgcct          50

<210> 122
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 122
acacctgggtt caaagatggg                                         20

<210> 123
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 123
taggaagagt tgctgaaggc acgg                                         24

<210> 124
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 124
ttgccttact caggtgctac                                         20

<210> 125
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
```

## oligonucleotide probe

<400> 125  
actcagcagt ggttaggaaag 20

<210> 126  
<211> 1210  
<212> DNA  
<213> Homo sapiens

<400> 126  
cagcgcgtgg ccggcgccgc tgggggaca gcatgagcgg cggttggatg ggcagggttg 60  
gagcgtggcg aacaggggct ctgggcctgg cgctgcgtct gctgctggc ctcggactag 120  
gcctggaggc cgccgcgagc cccgcttcca ccccacactc tgcccaggcc gcaggcccc 180  
gctcaaggctc gtggccaccc accaagttcc agtgcgcac cagtggctta tgcgtgcccc 240  
tcacctggcg ctgcgacagg gacttggact gcagcgatgg cagcgatgag gaggagtgca 300  
ggattgagcc atgtaccagg aaagggcaat gcccacccgc ccctggcctc ccctggccct 360  
gcaccggcgt cagtgaactgc tctggggaa ctgacaagaa actgcgcac ac tgcagccg 420  
tggcctgcct agcaggcgag ctccgttgca cgctgagcga tgactgcatt ccactcacgt 480  
ggcgcgtgcga cggccaccca gactgtcccg actccagcga cgagctcgcc tggaaacca 540  
atgagatcct cccggaaggg gatgccacaa ccatggggcc ccctgtgacc ctggagagtg 600  
tcacctctct caggaatgcc acaaccatgg ggccctgt gaccctggag agtgcctcc 660  
ctgtcgggaa tgccacatcc tcctctggc gagaccagtc tggaaagccca actgcctatg 720  
gggttattgc agctgctgct gtgtcagtg caagcctgtt caccgcacc ctccctttt 780  
tgtcctggct ccgagcccgag gagcgcctcc gcccactggg gttactggg gccatgaagg 840  
agtccctgtc gctgtcagaa cagaagaccc tgcgtccctg aggacaagca cttgcccacca 900  
ccgtcactca gcccctggcg tagccggaca ggaggagagc agtgatgcgg atgggtaccc 960  
gggcacacca gcccctcagag acctgagttc ttctggccac gtggaaacctc gaaccggc 1020  
tcctgcagaa gtggccctgg agattgaggg tccctggaca ctccctatgg agatccgggg 1080  
agcttaggatg gggAACCTGC cacagccaga actgaggggc tggcccccagg cagctcccag 1140  
gggttagaac gggccctgtgc ttaagacact ccctgctgccc ccgtctgagg gtggcgatta 1200  
aagttgcttc 1210

<210> 127  
<211> 282  
<212> PRT  
<213> Homo sapiens

<400> 127  
Met Ser Gly Gly Trp Met Ala Gln Val Gly Ala Trp Arg Thr Gly Ala  
1 5 10 15

Leu Gly Leu Ala Leu Leu Leu Leu Gly Leu Gly Leu Gly Leu Glu  
20 25 30

Ala Ala Ala Ser Pro Leu Ser Thr Pro Thr Ser Ala Gln Ala Ala Gly  
35 40 45

Pro Ser Ser Gly Ser Cys Pro Pro Thr Lys Phe Gln Cys Arg Thr Ser  
50 55 60

Gly Leu Cys Val Pro Leu Thr Trp Arg Cys Asp Arg Asp Leu Asp Cys  
65 70 75 80

Ser Asp Gly Ser Asp Glu Glu Glu Cys Arg Ile Glu Pro Cys Thr Gln  
 85 90 95

Lys Gly Gln Cys Pro Pro Pro Gly Leu Pro Cys Pro Cys Thr Gly  
 100 105 110

Val Ser Asp Cys Ser Gly Gly Thr Asp Lys Lys Leu Arg Asn Cys Ser  
 115 120 125

Arg Leu Ala Cys Leu Ala Gly Glu Leu Arg Cys Thr Leu Ser Asp Asp  
 130 135 140

Cys Ile Pro Leu Thr Trp Arg Cys Asp Gly His Pro Asp Cys Pro Asp  
 145 150 155 160

Ser Ser Asp Glu Leu Gly Cys Gly Thr Asn Glu Ile Leu Pro Glu Gly  
 165 170 175

Asp Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val Thr Ser  
 180 185 190

Leu Arg Asn Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val  
 195 200 205

Pro Ser Val Gly Asn Ala Thr Ser Ser Ser Ala Gly Asp Gln Ser Gly  
 210 215 220

Ser Pro Thr Ala Tyr Gly Val Ile Ala Ala Ala Ala Val Leu Ser Ala  
 225 230 235 240

Ser Leu Val Thr Ala Thr Leu Leu Leu Ser Trp Leu Arg Ala Gln  
 245 250 255

Glu Arg Leu Arg Pro Leu Gly Leu Leu Val Ala Met Lys Glu Ser Leu  
 260 265 270

Leu Leu Ser Glu Gln Lys Thr Ser Leu Pro  
 275 280

<210> 128

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 128

aagtccagt gccgcaccag tggc

24

<210> 129

6  
5  
4  
3  
2  
1

<211> 24  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe  
  
<400> 129  
ttggttccac agccgagctc gtcg 24  
  
<210> 130  
<211> 50  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe  
  
<400> 130  
gaggaggagt gcaggattga gccatgtacc cagaaaggc aatgccacc 50  
  
<210> 131  
<211> 1843  
<212> DNA  
<213> Homo sapiens  
  
<220>  
<221> modified\_base  
<222> (1837)  
<223> a, t, c or g  
  
<400> 131  
cccacgcgtc cggtctcgct cgctcgcgca gcggcgccag cagaggtcgc gcacagatgc 60  
gggttagact ggcgggggga ggaggcgag gagggaaagga agctgcattgc atgagaccca 120  
cagactcttg caagctggat gccccttgtg gatgaaaagat gtatcatgga atgaacccga 180  
gcaatggaga tggatttcta gagcagcagc agcagcagca gcaacctcag tccccccaga 240  
gactcttgc cgtgatctg tggtttcagc tggcgctgtg cttcgccct gcacagctca 300  
cggcggtt cgtgatctt caagtgtgtg ctgaccccg cattcccgag aatggcttc 360  
ggaccccccag cggagggggtt ttctttgaag gctctgttagc ccgatttcac tgccaagacg 420  
gattcaagct gaaggcgct acaaagagac tggatgttgc gcatatataat ggaaccttag 480  
gctggatccc aagtgataat tccatctgtg tgcaagaaga ttgccgtatc cctcaaatcg 540  
aagatgctga gattcataac aagacatata gacatggaga gaagctaatc atcactttgtc 600  
atgaaggatt caagatccgg taccccgacc tacacaatat ggtttcatta tgtcgcgatg 660  
atggAACGTG gaataatctg cccatctgtc aaggctgcct gagacctcta gcctttctta 720  
atggctatgt aaacatctt gagctccaga cctccttccc ggtggggact gtgatctcct 780  
atcgctgtt tcccgattt aaacttgatg ggtctcgta tcttgagtgc ttacaaaacc 840  
ttatctggtc gtccagccca ccccggtgcc ttgctctggc agcccaagtc tgtccactac 900  
ctccaaatggt gagtcacgga gattcgtct gccaccccg gcttggtag gctacaacc 960  
acggaactgt ggtggagtt tactgcgtc ctggctacag cctcaccaggc gactacaagt 1020  
acatcacctg ccagttatgaa gagtggttc cttcttatca agtctactgc atcaaatcg 1080  
agcaaacgtg gcccagcacc catgagaccc tcctgaccac gtggaaaggatt gtggcgatc 1140

cgccaaccag tgtgctgctg gtgctgtgc tcgtcatcct ggcaggatg ttccagacca 1200  
 agttcaaggc ccactttccc cccagggggc ctccccggag ttccagcagt gaccctgact 1260  
 ttgtggtgtt agacggcgtg cccgtcatgc tcccgctcta tgacgaagct gtgagtgccg 1320  
 gctttagtgc ctttaggcccc gggtacatgg cctctgtggg ccagggctgc cccttacccg 1380  
 tggacgacca gagcccccca gcataccccg gtcagggga cacggacaca ggcccagggg 1440  
 agtcagaaac ctgtgacagc gtctcaggtt cttctgagct gctccaaagt ctgtattcac 1500  
 ctcccggtg ccaagagagc acccaccctg ctteggacaa ccctgacata attgccagca 1560  
 cgccagagga ggtggcatcc accagcccag gcatccatca tgcccaactgg gtgttgc 1620  
 taagaaaactg attgattaaa aaatttccca aagtgtctg aagtgtctct tcaaatacat 1680  
 gttgatctgt ggagttgatt ccttccttc tcttggttt agacaaatgt aaacaaagct 1740  
 ctgatcctta aaattgttat gctgatagag tggtagggc tggaaagctt atcaagtcct 1800  
 gtttcttctt gacacagact gattaaaaat taaaagnaaa aaa 1843

<210> 132  
 <211> 490  
 <212> PRT  
 <213> Homo sapiens

<400> 132  
 Met Tyr His Gly Met Asn Pro Ser Asn Gly Asp Gly Phe Leu Glu Gln  
 1 5 10 15

Gln Gln Gln Gln Gln Gln Pro Gln Ser Pro Gln Arg Leu Leu Ala Val  
 20 25 30

Ile Leu Trp Phe Gln Leu Ala Leu Cys Phe Gly Pro Ala Gln Leu Thr  
 35 40 45

Gly Gly Phe Asp Asp Leu Gln Val Cys Ala Asp Pro Gly Ile Pro Glu  
 50 55 60

Asn Gly Phe Arg Thr Pro Ser Gly Gly Val Phe Phe Glu Gly Ser Val  
 65 70 75 80

Ala Arg Phe His Cys Gln Asp Gly Phe Lys Leu Lys Gly Ala Thr Lys  
 85 90 95

Arg Leu Cys Leu Lys His Phe Asn Gly Thr Leu Gly Trp Ile Pro Ser  
 100 105 110

Asp Asn Ser Ile Cys Val Gln Glu Asp Cys Arg Ile Pro Gln Ile Glu  
 115 120 125

Asp Ala Glu Ile His Asn Lys Thr Tyr Arg His Gly Glu Lys Leu Ile  
 130 135 140

Ile Thr Cys His Glu Gly Phe Lys Ile Arg Tyr Pro Asp Leu His Asn  
 145 150 155 160

Met Val Ser Leu Cys Arg Asp Asp Gly Thr Trp Asn Asn Leu Pro Ile  
 165 170 175

Cys Gln Gly Cys Leu Arg Pro Leu Ala Ser Ser Asn Gly Tyr Val Asn

180	185	190	
Ile Ser Glu Leu Gln Thr Ser Phe Pro Val Gly Thr Val Ile Ser Tyr			
195	200	205	
Arg Cys Phe Pro Gly Phe Lys Leu Asp Gly Ser Ala Tyr Leu Glu Cys			
210	215	220	
Leu Gln Asn Leu Ile Trp Ser Ser Ser Pro Pro Arg Cys Leu Ala Leu			
225	230	235	240
Glu Ala Gln Val Cys Pro Leu Pro Pro Met Val Ser His Gly Asp Phe			
245	250	255	
Val Cys His Pro Arg Pro Cys Glu Arg Tyr Asn His Gly Thr Val Val			
260	265	270	
Glu Phe Tyr Cys Asp Pro Gly Tyr Ser Leu Thr Ser Asp Tyr Lys Tyr			
275	280	285	
Ile Thr Cys Gln Tyr Gly Glu Trp Phe Pro Ser Tyr Gln Val Tyr Cys			
290	295	300	
Ile Lys Ser Glu Gln Thr Trp Pro Ser Thr His Glu Thr Leu Leu Thr			
305	310	315	320
Thr Trp Lys Ile Val Ala Phe Thr Ala Thr Ser Val Leu Leu Val Leu			
325	330	335	
Leu Leu Val Ile Leu Ala Arg Met Phe Gln Thr Lys Phe Lys Ala His			
340	345	350	
Phe Pro Pro Arg Gly Pro Pro Arg Ser Ser Ser Ser Asp Pro Asp Phe			
355	360	365	
Val Val Val Asp Gly Val Pro Val Met Leu Pro Ser Tyr Asp Glu Ala			
370	375	380	
Val Ser Gly Gly Leu Ser Ala Leu Gly Pro Gly Tyr Met Ala Ser Val			
385	390	395	400
Gly Gln Gly Cys Pro Leu Pro Val Asp Asp Gln Ser Pro Pro Ala Tyr			
405	410	415	
Pro Gly Ser Gly Asp Thr Asp Thr Gly Pro Gly Glu Ser Glu Thr Cys			
420	425	430	
Asp Ser Val Ser Gly Ser Ser Glu Leu Leu Gln Ser Leu Tyr Ser Pro			
435	440	445	
Pro Arg Cys Gln Glu Ser Thr His Pro Ala Ser Asp Asn Pro Asp Ile			
450	455	460	

Ile Ala Ser Thr Ala Glu Glu Val Ala Ser Thr Ser Pro Gly Ile His  
 465 470 475 480

His Ala His Trp Val Leu Phe Leu Arg Asn  
 485 490

<210> 133  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 133  
atctcctatac gctgctttcc cggt 23

<210> 134  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 134  
agccaggatc gcagtaaaac tcc 23

<210> 135  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 135  
atttaaactt gatgggtctg cgtatcttga gtgcttacaa aaccttatct 50

<210> 136  
<211> 1815  
<212> DNA  
<213> Homo sapiens

<400> 136  
ccccacgcgtc cgctccgcgc cctccccccc gcctcccgta cggtccgtcg gtggccataga 60  
gatgctgtcg ccgcgggtgc agttgtcgcg cacgcctctg cccgccagcc cgctccaccg 120  
ccgttagcgcc cgagtgtcgg ggggcgcacc cgagtccggc catgaggccg ggaaccgcgc 180  
tacaggccgt gctgctgccc gtgctgtcg tggtggctgcg gggccgcacg ggtcgcctgc 240  
tgagtgccctc ggatttggac ctcagaggag ggcagccagt ctgccgggaa gggacacaga 300

ggccttgtta taaagtcat tacttccatg atacttctcg aagactgaac tttgaggaag 360  
 ccaaagaagc ctgcaggagg gatggaggcc agctagtcg catcgagtct gaagatgaac 420  
 agaaaactgat agaaaagtcc attgaaaacc tcttgccatc tgatgggtac ttctggattg 480  
 ggctcaggag gcgtgaggag aaacaaagca atagcacagc ctgccaggac ctttatgctt 540  
 ggactgatgg cagcatatca caattttagga actggatgtt ggatgagccg tcctgcggca 600  
 gcgaggctg cgtggatcatg taccatcagc catcgccacc cgctggcatc ggaggcccct 660  
 acatgttcca gtggaatgat gaccgggtca acatgaagaa caatttcatt tgcaaataatt 720  
 ctgatgagaa accagcagtt cttcttagag aagctgaagg tgaggaaaca gagctgacaa 780  
 cacctgtact tccagaagaa acacaggaag aagatgccaa aaaaacattt aaagaaagta 840  
 gagaagctgc cttgaatctg gcctacatcc taatccccag cattccctt ctcctcctcc 900  
 ttgtggtcac cacagttgtt tttgggtttt ggatctgttag aaaaagaaaaa cgggagcagc 960  
 cagaccctag cacaagaag caacacacca tctggccctc tcctcaccag gaaaaacagcc 1020  
 cggacacctaga ggtctacaat gtcataagaa aacaaagcga agctgactta gctgagaccc 1080  
 ggccagacct gaagaatatt tcattcccgag tgtgttcggg agaagccact cccgatgaca 1140  
 tgtcttgtga ctatgacaac atggctgtga acccatcaga aagtgggtttt gtgactctgg 1200  
 tgagcgtgga gagtggattt gtgaccaatg acatttatga gttctcccca gaccaatgg 1260  
 ggaggagtaa ggagtctgga tgggtggaaa atgaaatata tggttattag gacatataaa 1320  
 aaactgaaac tgacaacaat ggaaaagaaaa tgataagcaa aatcctctta ttttctataa 1380  
 ggaaaataca cagaaggct atgaacaagc ttagatcagg tcctgtggat gagcatgtgg 1440  
 tccccacgac ctccctgtgg acccccacgt tttggctgta tcctttatcc cagccagtca 1500  
 tccagctcga ccttatgaga aggtaccttg cccaggtctg gcacatagta gagtctcaat 1560  
 aaatgtcaact tgggtggttt tatctaactt ttaagggaca gagctttacc tggcagtgtat 1620  
 aaagatgggc tggagacctt ggaaaaccac ctctgtttc ctgctctat acagcagcac 1680  
 atattatcat acagacagaa aatccagaat ctttcaaag cccacatatg gtagcacagg 1740  
 ttggcctgtg catcggaat tctcatatct gttttttca aagaataaaa tcaaataaaag 1800  
 agcaggaaaa aaaaaa 1815

&lt;210&gt; 137

&lt;211&gt; 382

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 137

Met	Arg	Pro	Gly	Thr	Ala	Leu	Gln	Ala	Val	Leu	Leu	Ala	Val	Leu	Leu
1					5				10				15		

Val	Gly	Leu	Arg	Ala	Ala	Thr	Gly	Arg	Leu	Leu	Ser	Ala	Ser	Asp	Leu
					20				25				30		

Asp	Leu	Arg	Gly	Gly	Gln	Pro	Val	Cys	Arg	Gly	Gly	Thr	Gln	Arg	Pro
					35			40				45			

Cys	Tyr	Lys	Val	Ile	Tyr	Phe	His	Asp	Thr	Ser	Arg	Arg	Leu	Asn	Phe
					50			55			60				

Glu	Glu	Ala	Lys	Glu	Ala	Cys	Arg	Arg	Asp	Gly	Gly	Gln	Leu	Val	Ser
					65			70			75		80		

Ile	Glu	Ser	Glu	Asp	Glu	Gln	Lys	Leu	Ile	Glu	Lys	Phe	Ile	Glu	Asn
					85			90				95			

Leu	Leu	Pro	Ser	Asp	Gly	Asp	Phe	Trp	Ile	Gly	Leu	Arg	Arg	Arg	Glu
					100			105				110			

Glu Lys Gln Ser Asn Ser Thr Ala Cys Gln Asp Leu Tyr Ala Trp Thr  
 115 120 125  
 Asp Gly Ser Ile Ser Gln Phe Arg Asn Trp Tyr Val Asp Glu Pro Ser  
 130 135 140  
 Cys Gly Ser Gln Val Cys Val Val Met Tyr His Gln Pro Ser Ala Pro  
 145 150 155 160  
 Ala Gly Ile Gly Gly Pro Tyr Met Phe Gln Trp Asn Asp Asp Arg Cys  
 165 170 175  
 Asn Met Lys Asn Asn Phe Ile Cys Lys Tyr Ser Asp Glu Lys Pro Ala  
 180 185 190  
 Val Pro Ser Arg Glu Ala Glu Gly Glu Glu Thr Glu Leu Thr Thr Pro  
 195 200 205  
 Val Leu Pro Glu Glu Thr Gln Glu Glu Asp Ala Lys Lys Thr Phe Lys  
 210 215 220  
 Glu Ser Arg Glu Ala Ala Leu Asn Leu Ala Tyr Ile Leu Ile Pro Ser  
 225 230 235 240  
 Ile Pro Leu Leu Leu Leu Val Val Thr Thr Val Val Cys Trp Val  
 245 250 255  
 Trp Ile Cys Arg Lys Arg Lys Arg Glu Gln Pro Asp Pro Ser Thr Lys  
 260 265 270  
 Lys Gln His Thr Ile Trp Pro Ser Pro His Gln Gly Asn Ser Pro Asp  
 275 280 285  
 Leu Glu Val Tyr Asn Val Ile Arg Lys Gln Ser Glu Ala Asp Leu Ala  
 290 295 300  
 Glu Thr Arg Pro Asp Leu Lys Asn Ile Ser Phe Arg Val Cys Ser Gly  
 305 310 315 320  
 Glu Ala Thr Pro Asp Asp Met Ser Cys Asp Tyr Asp Asn Met Ala Val  
 325 330 335  
 Asn Pro Ser Glu Ser Gly Phe Val Thr Leu Val Ser Val Glu Ser Gly  
 340 345 350  
 Phe Val Thr Asn Asp Ile Tyr Glu Phe Ser Pro Asp Gln Met Gly Arg  
 355 360 365  
 Ser Lys Glu Ser Gly Trp Val Glu Asn Glu Ile Tyr Gly Tyr  
 370 375 380

<211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 138  
 gttcattgaa aacctcttgc catctgatgg tgacttctgg attgggctca 50

<210> 139  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 139  
 aagccaaaga agcctgcagg aggg 24

<210> 140  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 140  
 cagtccaagc ataaagggtcc tggc 24

<210> 141  
 <211> 1514  
 <212> DNA  
 <213> Homo sapiens

<400> 141  
 ggggtctccc tcagggccgg gaggcacagc ggtccctgct tgctgaaggg ctggatgtac 60  
 gcatccgcag gttcccgccg acttgggggc gcccgttag ccccgccgcg cgcagaagac 120  
 ttgtgtttgc ctcctgcagc ctaaacccgg agggcagcga gggcttacca ccatgatcac 180  
 tgggtgttc agcatgcgtc tgtggacccc agtggcgctc ctgacactgc tggegtactg 240  
 cctgcaccag cggcggtgg ccctggccga gctgcaggag gccgatggcc agtgtccgg 300  
 cgaccgcagc ctgctgaagt taaaatggt gcaggtcgtg ttcgacacg gggctcggag 360  
 tcctctcaag ccgcctccgc tggaggagca ggttagagtgg aacccccacg tattagaggt 420  
 cccaccccaa actcagttt attacacagt caccaatcta gctgggtggtc cggaaaccata 480  
 ttctccttac gactctcaat accatgagac caccctgaag gggggcatgt ttgctggca 540  
 gctgaccaag gtgggcatgc agcaaatgtt tgccttgga gagagactga ggaagaacta 600  
 tgtgaaagac attcccttgc tttcaccaac cttcaacccca caggaggtct ttattcggtc 660  
 cactaacatt tttcggatc tggagtccac ccgttggc ctggctggc tttccagtg 720

tcagaaagaa ggacccatca tcatccacac tcatgaagca gattcagaag tcttgatcc 780  
 caactaccaa agctgctgga gcctgaggca gagaaccaga gcccggaggc agactgcctc 840  
 tttacagcca ggaatctcg aggattgaa aaaggtaag gacaggatgg gcattgacag 900  
 tagtgataaa gtggacttct tcatcctcct ggacacaacgtg gctgccgagc aggcacacaa 960  
 cctcccaagc tgccccatgc tgaagagatt tgcacggatg atcgaacaga gagctgtgga 1020  
 cacatccttg tacatactgc ccaaggaaga cagggaaagt cttcagatgg cagtaggccc 1080  
 attcctccac atcctagaga gcaacctgct gaaagccatg gactctgcca ctgccccga 1140  
 caagatcaga aagctgtatc tctatgcggc tcatgatgtg accttcatac cgctcttaat 1200  
 gaccctgggg attttgacc acaaatggcc accgtttgtt gttgacctga ccatgaaact 1260  
 ttaccagcac ctgaaatcta aggagtggtt tgtcagctc tattaccacg ggaaggagca 1320  
 ggtgccgaga ggttgcctg atggctctg cccgctggac atgttcttga atgccatgtc 1380  
 agtttatacc ttaagccag aaaaatacca tgcactctgc tctcaaactc aggtgatgga 1440  
 agttgaaat gaagagtaac tgatttataa aagcaggatg tttgatttt aaaataaaagt 1500  
 gccttataac aatg 1514

<210> 142

<211> 428

<212> PRT

<213> Homo sapiens

<400> 142

Met	Ile	Thr	Gly	Val	Phe	Ser	Met	Arg	Leu	Trp	Thr	Pro	Val	Gly	Val
1							5				10				15

Leu	Thr	Ser	Leu	Ala	Tyr	Cys	Leu	His	Gln	Arg	Arg	Val	Ala	Leu	Ala
							20				25				30

Glu	Leu	Gln	Glu	Ala	Asp	Gly	Gln	Cys	Pro	Val	Asp	Arg	Ser	Leu	Leu
							35			40				45	

Lys	Leu	Lys	Met	Val	Gln	Val	Val	Phe	Arg	His	Gly	Ala	Arg	Ser	Pro
							50			55				60	

Leu	Lys	Pro	Leu	Pro	Leu	Glu	Glu	Gln	Val	Glu	Trp	Asn	Pro	Gln	Leu
							65			70				75	80

Leu	Glu	Val	Pro	Pro	Gln	Thr	Gln	Phe	Asp	Tyr	Thr	Val	Thr	Asn	Leu
							85			90				95	

Ala	Gly	Gly	Pro	Lys	Pro	Tyr	Ser	Pro	Tyr	Asp	Ser	Gln	Tyr	His	Glu
							100			105				110	

Thr	Thr	Leu	Lys	Gly	Gly	Met	Phe	Ala	Gly	Gln	Leu	Thr	Lys	Val	Gly
						115			120				125		

Met	Gln	Gln	Met	Phe	Ala	Leu	Gly	Glu	Arg	Leu	Arg	Lys	Asn	Tyr	Val
							130			135				140	

Glu	Asp	Ile	Pro	Phe	Leu	Ser	Pro	Thr	Phe	Asn	Pro	Gln	Glu	Val	Phe
							145			150				155	160

Ile	Arg	Ser	Thr	Asn	Ile	Phe	Arg	Asn	Leu	Glu	Ser	Thr	Arg	Cys	Leu
							165			170				175	

Leu Ala Gly Leu Phe Gln Cys Gln Lys Glu Gly Pro Ile Ile Ile His  
           180                 185                 190

Thr Asp Glu Ala Asp Ser Glu Val Leu Tyr Pro Asn Tyr Gln Ser Cys  
           195                 200                 205

Trp Ser Leu Arg Gln Arg Thr Arg Gly Arg Arg Gln Thr Ala Ser Leu  
           210                 215                 220

Gln Pro Gly Ile Ser Glu Asp Leu Lys Lys Val Lys Asp Arg Met Gly  
           225                 230                 235                 240

Ile Asp Ser Ser Asp Lys Val Asp Phe Phe Ile Leu Leu Asp Asn Val  
           245                 250                 255

Ala Ala Glu Gln Ala His Asn Leu Pro Ser Cys Pro Met Leu Lys Arg  
           260                 265                 270

Phe Ala Arg Met Ile Glu Gln Arg Ala Val Asp Thr Ser Leu Tyr Ile  
           275                 280                 285

Leu Pro Lys Glu Asp Arg Glu Ser Leu Gln Met Ala Val Gly Pro Phe  
           290                 295                 300

Leu His Ile Leu Glu Ser Asn Leu Leu Lys Ala Met Asp Ser Ala Thr  
           305                 310                 315                 320

Ala Pro Asp Lys Ile Arg Lys Leu Tyr Leu Tyr Ala Ala His Asp Val  
           325                 330                 335

Thr Phe Ile Pro Leu Leu Met Thr Leu Gly Ile Phe Asp His Lys Trp  
           340                 345                 350

Pro Pro Phe Ala Val Asp Leu Thr Met Glu Leu Tyr Gln His Leu Glu  
           355                 360                 365

Ser Lys Glu Trp Phe Val Gln Leu Tyr Tyr His Gly Lys Glu Gln Val  
           370                 375                 380

Pro Arg Gly Cys Pro Asp Gly Leu Cys Pro Leu Asp Met Phe Leu Asn  
           385                 390                 395                 400

Ala Met Ser Val Tyr Thr Leu Ser Pro Glu Lys Tyr His Ala Leu Cys  
           405                 410                 415

Ser Gln Thr Gln Val Met Glu Val Gly Asn Glu Glu  
           420                 425

<210> 143  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 143  
ccaactacca aagctgctgg agcc 24

<210> 144  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 144  
gcagctctat taccacggga agga 24

<210> 145  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 145  
tccttcccgt ggtaatagag ctgc 24

<210> 146  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 146  
ggcagagaac cagaggccgg aggagactgc ctctttacag ccagg 45

<210> 147  
<211> 1686  
<212> DNA  
<213> Homo sapiens

<400> 147  
ctcctcttaa catacttgca gctaaaacta aatattgctg cttggggacc tccttctagc 60  
cttaaatttc agctcatcac cttcacctgc cttggtcatg gctctgctat ttccttgc 120  
ccttgccatt tgcaccagac ctggattcct agcgtctcca tctggagtgc ggctgggtggg 180



Asp Cys Ser His Asp Glu Asp Ala Gly Ala Ser Cys Glu Asn Pro Glu  
 115 120 125

Ser Ser Phe Ser Pro Val Pro Glu Gly Val Arg Leu Ala Asp Gly Pro  
 130 135 140

Gly His Cys Lys Gly Arg Val Glu Val Lys His Gln Asn Gln Trp Tyr  
 145 150 155 160

Thr Val Cys Gln Thr Gly Trp Ser Leu Arg Ala Ala Lys Val Val Cys  
 165 170 175

Arg Gln Leu Gly Cys Gly Arg Ala Val Leu Thr Gln Lys Arg Cys Asn  
 180 185 190

Lys His Ala Tyr Gly Arg Lys Pro Ile Trp Leu Ser Gln Met Ser Cys  
 195 200 205

Ser Gly Arg Glu Ala Thr Leu Gln Asp Cys Pro Ser Gly Pro Trp Gly  
 210 215 220

Lys Asn Thr Cys Asn His Asp Glu Asp Thr Trp Val Glu Cys Glu Asp  
 225 230 235 240

Pro Phe Asp Leu Arg Leu Val Gly Gly Asp Asn Leu Cys Ser Gly Arg  
 245 250 255

Leu Glu Val Leu His Lys Gly Val Trp Gly Ser Val Cys Asp Asp Asn  
 260 265 270

Trp Gly Glu Lys Glu Asp Gln Val Val Cys Lys Gln Leu Gly Cys Gly  
 275 280 285

Lys Ser Leu Ser Pro Ser Phe Arg Asp Arg Lys Cys Tyr Gly Pro Gly  
 290 295 300

Val Gly Arg Ile Trp Leu Asp Asn Val Arg Cys Ser Gly Glu Glu Gln  
 305 310 315 320

Ser Leu Glu Gln Cys Gln His Arg Phe Trp Gly Phe His Asp Cys Thr  
 325 330 335

His Gln Glu Asp Val Ala Val Ile Cys Ser Val  
 340 345

<210> 149  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic

FBI Laboratory

## oligonucleotide probe

<400> 149		
ttcagctcat cacccatccc tgcc		24
<210> 150		
<211> 24		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		
<400> 150		
ggctcataca aaataaccact aggg		24
<210> 151		
<211> 50		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		
<400> 151		
gggcctccac cgctgtgaag ggccgggtgaa ggtggaaacag aaaggccagt		50
<210> 152		
<211> 1427		
<212> DNA		
<213> Homo sapiens		
<400> 152		
actgcactcg gttctatcgta ttgaattccc cggggatccct cttagatcc ctcgaccccg 60		
acccacgcgt ccgcggacgc gtggggcgac gcgtggcccg gctaccagga agagtctgcc 120		
gaaggtgaag gccatggact tcatacaccc cacagccatc ctgcccctgc tggtcggtcg 180		
cctggcgctc ttccggctct tccggctgt gcagtgggtg cgccggaaagg cctacctcg 240		
aatgtctgtg gtgggtatca caggcgccac ctcaggctg ggcaaaagaat gtgaaaagg 300		
cttctatgtc gcgggtgtcta aactgggtgt ctgtggccgg aatgggtgggg ccctagaaga 360		
gctcatcaga gaacttaccg cttctcatgc caccaagggtg cagacacaca agccttactt 420		
ggtgacccctc gacccatcag actctggggc catagttgca gcagcagctg agatcctgca 480		
gtgccttggc tatgtcgaca tacttgtcaa caatgtctggg atcagactacc gtggtaccat 540		
catggacacc acagtggatg tggacaagag ggtcatggag acaaactact ttggcccaagt 600		
tgcctctaacc aaaggactcc tgcctccat gatcaagagg aggcaaggcc acattgtcg 660		
catcaggcgc atccaggcga agatgagcat tcctttcgatc tcagcatatcg cagccctccaa 720		
gcacgcacc caggctttct ttgactgtct gcgtggccag atggaaacagt atgaaattgaa 780		
ggtgaccgtc atcagccccg gctacatcca caccaacccctc tctgttaaatcg ccatcaccgc 840		
ggatggatct aggtatggag ttatggacac caccacagcc cagggccgaa gccctgtgaa 900		
ggtgcccaag gatgttcttgc ctgtgtggg gaagaagaag aaagatgtga tcctggctga 960		
cttactgcct tccttggctg ttatcttcg aactctggct cctggccctc tcttcagcc 1020		
catggcctcc aaggccagaa aagagcggaa atccaaagaac tccttagtact ctgaccagcc 1080		

agggccaggg cagagaagca gcactcttag gcttgcttac tctacaaggg acagttgcac 1140  
 ttgttgagac ttaatggag atttgtctca caagtggaa agactgaaga aacacatctc 1200  
 gtgcagatct gctggcagag gacaatcaa aacgacaaca agcttcttcc cagggtgagg 1260  
 gaaaaacactt aaggaataaa tatggagctg gggtaaca ctaaaaacta gaaataaaca 1320  
 tctcaaacag taaaaaaaaaaa aaaaaaggc ggccgcgact ctagagtcga cctgcagaag 1380  
 cttggccgcc atggcccaac ttgttattt cagttataa tgttac 1427

<210> 153

<211> 310

<212> PRT

<213> Homo sapiens

<400> 153

Met	Asp	Phe	Ile	Thr	Ser	Thr	Ala	Ile	Leu	Pro	Leu	Leu	Phe	Gly	Cys
1															15

5

10

Leu	Gly	Val	Phe	Gly	Leu	Phe	Arg	Leu	Leu	Gln	Trp	Val	Arg	Gly	Lys
															30

20

25

Ala	Tyr	Leu	Arg	Asn	Ala	Val	Val	Val	Ile	Thr	Gly	Ala	Thr	Ser	Gly
															45

35

40

Leu	Gly	Lys	Glu	Cys	Ala	Lys	Val	Phe	Tyr	Ala	Ala	Gly	Ala	Lys	Leu
															60

50

55

Val	Leu	Cys	Gly	Arg	Asn	Gly	Gly	Ala	Leu	Glu	Glu	Leu	Ile	Arg	Glu
															80

65

70

75

80

Leu	Thr	Ala	Ser	His	Ala	Thr	Lys	Val	Gln	Thr	His	Lys	Pro	Tyr	Leu
															95

85

90

95

Val	Thr	Phe	Asp	Leu	Thr	Asp	Ser	Gly	Ala	Ile	Val	Ala	Ala	Ala	
															110

100

105

110

Glu	Ile	Leu	Gln	Cys	Phe	Gly	Tyr	Val	Asp	Ile	Leu	Val	Asn	Asn	Ala
															125

115

120

125

Gly	Ile	Ser	Tyr	Arg	Gly	Thr	Ile	Met	Asp	Thr	Thr	Val	Asp	Val	Asp
															130

130

135

140

Lys	Arg	Val	Met	Glu	Thr	Asn	Tyr	Phe	Gly	Pro	Val	Ala	Leu	Thr	Lys
															145

145

150

155

160

Ala	Leu	Leu	Pro	Ser	Met	Ile	Lys	Arg	Arg	Gln	Gly	His	Ile	Val	Ala
															165

165

170

175

Ile	Ser	Ser	Ile	Gln	Gly	Lys	Met	Ser	Ile	Pro	Phe	Arg	Ser	Ala	Tyr
															180

180

185

190

Ala	Ala	Ser	Lys	His	Ala	Thr	Gln	Ala	Phe	Phe	Asp	Cys	Leu	Arg	Ala
															195

195

200

205

Glu Met Glu Gln Tyr Glu Ile Glu Val Thr Val Ile Ser Pro Gly Tyr

210	215	220
Ile His Thr Asn Leu Ser Val Asn Ala Ile Thr Ala Asp Gly Ser Arg		
225	230	235
Tyr Gly Val Met Asp Thr Thr Ala Gln Gly Arg Ser Pro Val Glu		
245	250	255
Val Ala Gln Asp Val Leu Ala Ala Val Gly Lys Lys Lys Asp Val		
260	265	270
Ile Leu Ala Asp Leu Leu Pro Ser Leu Ala Val Tyr Leu Arg Thr Leu		
275	280	285
Ala Pro Gly Leu Phe Phe Ser Leu Met Ala Ser Arg Ala Arg Lys Glu		
290	295	300
Arg Lys Ser Lys Asn Ser		
305	310	

<210> 154  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 154  
ggtgctaaac tggtgctctg tggc 24

<210> 155  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 155  
cagggcaaga tgaggcatcc 20

<210> 156  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 156		
tcatactgtt ccatctcgcc acgc		24
<210> 157		
<211> 50		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		
<400> 157		
aatgggtggg ccctagaaga gctcatcaga gaactcaccg cttctcatgc		50
<210> 158		
<211> 1771		
<212> DNA		
<213> Homo sapiens		
<400> 158		
ccccacgcgtc cgctgggtt agatcgagca accctctaaa agcagtttag agtggtaaaa 60 aaaaaaaaaa acacaccaaa cgctcgacg cacaaggatgaaatttc ttctggacat 120 cctcctgtt ctcccggttac tgatcgctg ctccctagag tccttcgtga agctttttat 180 tcctaagagg agaaaatcag tcaccggcga aatcgctg attacaggag ctgggcattgg 240 aattgggaga ctgactgcct atgaatttgc taaacttaaa agcaagctgg ttctctggga 300 tataaataag catggactgg agggaaacagc tgccaaatgc aaggactgg gtgccaaggt 360 tcataccctt gtggtagact gcagcaaccc agaagatatt tacagctctg caaagaaggt 420 gaaggcagaa attggagatg ttagtatttt agtaaataat gctggtagt tagtatacatc 480 agatttgtt gctacacaag atcctcagat tgaaaagact tttgaagttt atgtacttgc 540 acatttctgg actacaaagg catttctcc tgcaatgacg aagaataacc atggccatat 600 tgtcaactgtg gcttcggcag ctggacatgt ctcggcccc ttcttactgg cttactgttc 660 aagcaagttt gctgctgtt gattcataa aactttgaca gatgaactgg ctgccttaca 720 aataactgga gtcaaaacaa catgtctgtc tcctaatttc gtaaacactg gcttcatcaa 780 aaatccaagt acaagtttg gaccactct ggaacctgag gaagtggtaa acaggctgat 840 gcatgggatt ctgactgagc agaagatgat ttttattcca tcttctatag ctttttaac 900 aacattggaa aggatccttc ctgagcgtt cctggcagtt taaaacgaa aaatcagtgt 960 taagtttgc gcaattttt gatataaaat gaaagcgtaa taagcaccta gtttctgaa 1020 aactgattt ccaggtttt gtttgcgtca tctaattttt ccagaattttt aatgtttgaa 1080 cttctgttt ttcttaattt cccatttct tcaatatcat ttttggggct ttggcagtct 1140 tcatttacta ccacttggc ttttagccaa agctgattac atatgatata aacagagaaa 1200 tacctttaga ggtgacttta agaaaaatga agaaaaagaa ccaaaatgac tttttaaaaa 1260 taatttccaa gattattttt ggctcacctg aaggcttgc aaaatttgc ccataaccgt 1320 ttatttaaca tatattttt ttttgcgtt cacttaattt ttgttataatt tttttttttt 1380 tttctgtttt acataaaatc agaaaacttca agctctctaa ataaaatgaa ggactatatc 1440 tagtggattt tcacaatgaa tatcatgaac tctcaatggg tagtttcat cctaccatt 1500 gccactctgt ttcctgagag atacactaca ttccaaatgcc aaacatttct gcacagggaa 1560 gcttagaggtg gatacacgtt ttgcaagttt aaaagcatca ctgggattta aggagaattt 1620 agagaatgtt cccacaaatg gcagcaataa taaatggatc acacttaaaa aaaaaaaaaaa 1680 aaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa 1740 aaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa 1771		
<210> 159		

&lt;211&gt; 300

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 159

Met	Lys	Phe	Leu	Leu	Asp	Ile	Leu	Leu	Leu	Leu	Pro	Leu	Leu	Ile	Val
1						5					10				15

Cys	Ser	Leu	Glu	Ser	Phe	Val	Lys	Leu	Phe	Ile	Pro	Lys	Arg	Arg	Lys
							20			25				30	

Ser	Val	Thr	Gly	Glu	Ile	Val	Leu	Ile	Thr	Gly	Ala	Gly	His	Gly	Ile
							35			40				45	

Gly	Arg	Leu	Thr	Ala	Tyr	Glu	Phe	Ala	Lys	Leu	Lys	Ser	Lys	Leu	Val
						50			55		60				

Leu	Trp	Asp	Ile	Asn	Lys	His	Gly	Leu	Glu	Glu	Thr	Ala	Ala	Lys	Cys
						65		70		75				80	

Lys	Gly	Leu	Gly	Ala	Lys	Val	His	Thr	Phe	Val	Val	Asp	Cys	Ser	Asn
						85			90				95		

Arg	Glu	Asp	Ile	Tyr	Ser	Ser	Ala	Lys	Lys	Val	Lys	Ala	Glu	Ile	Gly
							100		105				110		

Asp	Val	Ser	Ile	Leu	Val	Asn	Asn	Ala	Gly	Val	Val	Tyr	Thr	Ser	Asp
						115			120			125			

Leu	Phe	Ala	Thr	Gln	Asp	Pro	Gln	Ile	Glu	Lys	Thr	Phe	Glu	Val	Asn
						130		135		140					

Val	Leu	Ala	His	Phe	Trp	Thr	Thr	Lys	Ala	Phe	Leu	Pro	Ala	Met	Thr
						145		150		155				160	

Lys	Asn	Asn	His	Gly	His	Ile	Val	Thr	Val	Ala	Ser	Ala	Ala	Gly	His
						165			170				175		

Val	Ser	Val	Pro	Phe	Leu	Leu	Ala	Tyr	Cys	Ser	Ser	Lys	Phe	Ala	Ala
						180		185				190			

Val	Gly	Phe	His	Lys	Thr	Leu	Thr	Asp	Glu	Leu	Ala	Ala	Leu	Gln	Ile
						195		200				205			

Thr	Gly	Val	Lys	Thr	Thr	Cys	Leu	Cys	Pro	Asn	Phe	Val	Asn	Thr	Gly
						210		215			220				

Phe	Ile	Lys	Asn	Pro	Ser	Thr	Ser	Leu	Gly	Pro	Thr	Leu	Glu	Pro	Glu
						225		230		235			240		

Glu	Val	Val	Asn	Arg	Leu	Met	His	Gly	Ile	Leu	Thr	Glu	Gln	Lys	Met
						245		250				255			

Ile Phe Ile Pro Ser Ser Ile Ala Phe Leu Thr Thr Leu Glu Arg Ile  
 260 265 270

Leu Pro Glu Arg Phe Leu Ala Val Leu Lys Arg Lys Ile Ser Val Lys  
 275 280 285

Phe Asp Ala Val Ile Gly Tyr Lys Met Lys Ala Gln  
 290 295 300

<210> 160

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 160

ggtaaggca gaaattggag atg

23

<210> 161

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 161

atcccatgca tcagcctgtt tacc

24

<210> 162

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 162

gctggtag tctatacatc agatttgttt gctacacaag atcctcag

48

<210> 163

<211> 2076

<212> DNA

<213> Homo sapiens

<400> 163

ccccacgcgtc cgcggacgcg tgggtcgact agttctagat cgcgagcgcc cgcccgccgc 60  
 tcagggagga gcaccgactg cgccgcaccc tgagagatgg ttgggtgccat gtggaaagg 120

tttgttcgc tggcctgtt gatgcctggc ccctgtgatg ggctgtttcg ctcccataac 180  
agaagtgtt ccatgccacc taagggagac tcaggacagc cattatttct cacccttac 240  
attgaagctg ggaagatcca aaaaggaaga gaattgagtt tggtcgcccc tttcccaagga 300  
ctgaacatga agagttatgc cggcttcctc accgtgaata agacttacaa cagcaacctc 360  
tttctcttgt tcttcccagc tcagatacag ccagaagatg ccccaagtatg tctctggcta 420  
cagggtggc cgggaggtt atccatgtt ggactctttg tggaacatgg gccttatgtt 480  
gtcacaagta acatgacctt gcgtgacaga gacttccccct ggaccacaac gctctccatg 540  
ctttacattt acaatccagt gggcacaggc tttagtttta ctgatgatac ccacggat 600  
gcagtcaatg aggacgatgt agcacggat ttatacagtg cactaattca gttttccag 660  
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qaaataaaaaa tattatataat aaaagtaaaa aaaaaaa 2076

<210> 164

<211> 476

<212> PRT

<213> Homo sapiens

<400> 164

Met Val Gly Ala Met Trp Lys Val Ile Val Ser Leu Val Leu Leu Met  
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Pro Gly Pro Cys Asp Gly Leu Phe Arg Ser Leu Tyr Arg Ser Val Ser  
20 25 30

Met Pro Pro Lys Gly Asp Ser Gly Gln Pro Leu Phe Leu Thr Pro Tyr  
                  35                  40                  45

Ile Glu Ala Gly Lys Ile Gln Lys Gly Arg Glu Leu Ser Leu Val Gly  
50 55 60

Pro Phe Pro Gly Leu Asn Met Lys Ser Tyr Ala Gly Phe Leu Thr Val

65	70	75	80
Asn Lys Thr Tyr Asn Ser Asn Leu Phe Phe Trp Phe Pro Ala Gln			
85		90	95
Ile Gln Pro Glu Asp Ala Pro Val Val Leu Trp Leu Gln Gly Gly Pro			
100		105	110
Gly Gly Ser Ser Met Phe Gly Leu Phe Val Glu His Gly Pro Tyr Val			
115		120	125
Val Thr Ser Asn Met Thr Leu Arg Asp Arg Asp Phe Pro Trp Thr Thr			
130		135	140
Thr Leu Ser Met Leu Tyr Ile Asp Asn Pro Val Gly Thr Gly Phe Ser			
145		150	155
Phe Thr Asp Asp Thr His Gly Tyr Ala Val Asn Glu Asp Asp Val Ala			
165		170	175
Arg Asp Leu Tyr Ser Ala Leu Ile Gln Phe Phe Gln Ile Phe Pro Glu			
180		185	190
Tyr Lys Asn Asn Asp Phe Tyr Val Thr Gly Glu Ser Tyr Ala Gly Lys			
195		200	205
Tyr Val Pro Ala Ile Ala His Leu Ile His Ser Leu Asn Pro Val Arg			
210		215	220
Glu Val Lys Ile Asn Leu Asn Gly Ile Ala Ile Gly Asp Gly Tyr Ser			
225		230	235
Asp Pro Glu Ser Ile Ile Gly Gly Tyr Ala Glu Phe Leu Tyr Gln Ile			
245		250	255
Gly Leu Leu Asp Glu Lys Gln Lys Tyr Phe Gln Lys Gln Cys His			
260		265	270
Glu Cys Ile Glu His Ile Arg Lys Gln Asn Trp Phe Glu Ala Phe Glu			
275		280	285
Ile Leu Asp Lys Leu Leu Asp Gly Asp Leu Thr Ser Asp Pro Ser Tyr			
290		295	300
Phe Gln Asn Val Thr Gly Cys Ser Asn Tyr Tyr Asn Phe Leu Arg Cys			
305		310	315
Thr Glu Pro Glu Asp Gln Leu Tyr Tyr Val Lys Phe Leu Ser Leu Pro			
325		330	335
Glu Val Arg Gln Ala Ile His Val Gly Asn Gln Thr Phe Asn Asp Gly			
340		345	350

Thr Ile Val Glu Lys Tyr Leu Arg Glu Asp Thr Val Gln Ser Val Lys  
 355 360 365

Pro Trp Leu Thr Glu Ile Met Asn Asn Tyr Lys Val Leu Ile Tyr Asn  
 370 375 380

Gly Gln Leu Asp Ile Ile Val Ala Ala Ala Leu Thr Glu Arg Ser Leu  
 385 390 395 400

Met Gly Met Asp Trp Lys Gly Ser Gln Glu Tyr Lys Lys Ala Glu Lys  
 405 410 415

Lys Val Trp Lys Ile Phe Lys Ser Asp Ser Glu Val Ala Gly Tyr Ile  
 420 425 430

Arg Gln Ala Gly Asp Phe His Gln Val Ile Ile Arg Gly Gly His  
 435 440 445

Ile Leu Pro Tyr Asp Gln Pro Leu Arg Ala Phe Asp Met Ile Asn Arg  
 450 455 460

Phe Ile Tyr Gly Lys Gly Trp Asp Pro Tyr Val Gly  
 465 470 475

<210> 165

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 165

ttccatgccca cctaaggag actc

24

<210> 166

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 166

tggatgaggt gtgcaatggc tggc

24

<210> 167

<211> 24

<212> DNA

<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 167
agctctcaga ggctggtcat aggg

<210> 168
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 168
gtcggccctt tcccaggact gaacatgaag agttatgccc gcttcctcac      50

<210> 169
<211> 2477
<212> DNA
<213> Homo sapiens

<400> 169
cgaggcgttt tccggctccg qaatggcaca tggggaaatc ccagtcttgt tggctacaac 60
atttttccct ttcctaacaa gttctaacag ctgttctaac agcttagtgat caggggttct 120
tcttgctgga gaagaaaaggc ctgaggggcag agcagggcac tctcaactcag ggtgaccagc 180
tccttgccctc tctgtggata acagagcatg agaaaagtcaa gagatgcagc ggagtgaggt 240
gatggaaagtc taaaatagga aggaattttg tggcaataat cagactctgg gagcagttga 300
cctggagagc ctgggggagg gcctgcctaa caagcttca aaaaacagga gcgacttcca 360
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acatctgcaa aagcaaa 2477

<210> 170

<211> 552

<212> PRT

<213> Homo sapiens

<400> 170

Met Gly Thr Leu Gly Gln Ala Ser Leu Phe Ala Pro Pro Gly Asn Tyr  
 1 5 10 15

Phe Trp Ser Asp His Ser Ala Leu Cys Phe Ala Glu Ser Cys Glu Gly  
20 25 30

Gln Pro Gly Lys Val Glu Gln Met Ser Thr His Arg Ser Arg Leu Leu  
35 40 45

Thr Ala Ala Pro Leu Ser Met Glu Gln Arg Gln Pro Trp Pro Arg Ala  
50 55 60

Leu Glu Val Asp Ser Arg Ser Val Val Leu Leu Ser Val Val Val Trp Val  
65 70 75 80

Leu Leu Ala Pro Pro Ala Ala Gly Met Pro Gln Phe Ser Thr Phe His  
85 90 95

Ser Glu Asn Arg Asp Trp Thr Phe Asn His Leu Thr Val His Gln Gly  
           100                 105                 110

Thr Gly Ala Val Tyr Val Gly Ala Ile Asn Arg Val Tyr Lys Leu Thr  
115 120 125

Gly Asn Leu Thr Ile Gln Val Ala His Lys Thr Gly Pro Glu Glu Asp  
130 135 140

Asn	Lys	Ser	Arg	Tyr	Pro	Pro	Leu	Ile	Val	Gln	Pro	Cys	Ser	Glu	Val
145					150					155					160

Leu Thr Leu Thr Asn Asn Val Asn Lys Leu Leu Ile Ile Asp Tyr Ser  
165 170 175

Glu Asn Arg Leu Leu Ala Cys Gly Ser Leu Tyr Gln Gly Val Cys Lys  
 180 185 190

Leu Leu Arg Leu Asp Asp Leu Phe Ile Leu Val Glu Pro Ser His Lys  
 195 200 205

Lys Glu His Tyr Leu Ser Ser Val Asn Lys Thr Gly Thr Met Tyr Gly  
 210 215 220

Val Ile Val Arg Ser Glu Gly Glu Asp Gly Lys Leu Phe Ile Gly Thr  
 225 230 235 240

Ala Val Asp Gly Lys Gln Asp Tyr Phe Pro Thr Leu Ser Ser Arg Lys  
 245 250 255

Leu Pro Arg Asp Pro Glu Ser Ser Ala Met Leu Asp Tyr Glu Leu His  
 260 265 270

Ser Asp Phe Val Ser Ser Leu Ile Lys Ile Pro Ser Asp Thr Leu Ala  
 275 280 285

Leu Val Ser His Phe Asp Ile Phe Tyr Ile Tyr Gly Phe Ala Ser Gly  
 290 295 300

Gly Phe Val Tyr Phe Leu Thr Val Gln Pro Glu Thr Pro Glu Gly Val  
 305 310 315 320

Ala Ile Asn Ser Ala Gly Asp Leu Phe Tyr Thr Ser Arg Ile Val Arg  
 325 330 335

Leu Cys Lys Asp Asp Pro Lys Phe His Ser Tyr Val Ser Leu Pro Phe  
 340 345 350

Gly Cys Thr Arg Ala Gly Val Glu Tyr Arg Leu Leu Gln Ala Ala Tyr  
 355 360 365

Leu Ala Lys Pro Gly Asp Ser Leu Ala Gln Ala Phe Asn Ile Thr Ser  
 370 375 380

Gln Asp Asp Val Leu Phe Ala Ile Phe Ser Lys Gly Gln Lys Gln Tyr  
 385 390 395 400

His His Pro Pro Asp Asp Ser Ala Leu Cys Ala Phe Pro Ile Arg Ala  
 405 410 415

Ile Asn Leu Gln Ile Lys Glu Arg Leu Gln Ser Cys Tyr Gln Gly Glu  
 420 425 430

Gly Asn Leu Glu Leu Asn Trp Leu Leu Gly Lys Asp Val Gln Cys Thr  
 435 440 445

Lys Ala Pro Val Pro Ile Asp Asp Asn Phe Cys Gly Leu Asp Ile Asn

450	455	460
Gln Pro Leu Gly Gly Ser Thr Pro Val Glu Gly Leu Thr Leu Tyr Thr		
465	470	475
480		
Thr Ser Arg Asp Arg Met Thr Ser Val Ala Ser Tyr Val Tyr Asn Gly		
485	490	495
Tyr Ser Val Val Phe Val Gly Thr Lys Ser Gly Lys Leu Lys Lys Val		
500	505	510
Arg Val Tyr Glu Phe Arg Cys Ser Asn Ala Ile His Leu Leu Ser Lys		
515	520	525
Glu Ser Leu Leu Glu Gly Ser Tyr Trp Trp Arg Phe Asn Tyr Arg Gln		
530	535	540
Leu Tyr Phe Leu Gly Glu Gln Arg		
545	550	

<210> 171  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
       oligonucleotide probe

<400> 171  
 tggaataccg cctcctgcag 20

<210> 172  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
       oligonucleotide probe

<400> 172  
 cttctgccct ttggagaaga tggc 24

<210> 173  
 <211> 43  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
       oligonucleotide probe

<400> 173  
 ggactcactg gcccaggcct tcaatatcac cagccaggac gat 42  
  
 <210> 174  
 <211> 3106  
 <212> DNA  
 <213> Homo sapiens  
  
 <220>  
 <221> modified\_base  
 <222> (1683)  
 <223> a, t, c or g  
  
 <400> 174  
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<210> 175

<211> 636

<212> PRT

<213> Homo sapiens

<220>

<221> MOD\_RES

<222> (539)

<223> Any amino acid

<400> 175

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20 25 30

Ser Thr Leu Val Pro Leu Arg Leu Arg His Arg Gln Leu Gly Leu Gln  
35 40 45

Ala Lys Gly Trp Asn Phe Met Leu Glu Asp Ser Thr Phe Trp Ile Phe  
50 55 60

Gly Gly Ser Ile His Tyr Phe Arg Val Pro Arg Glu Tyr Trp Arg Asp  
65 70 75 80

Arg Leu Leu Lys Met Lys Ala Cys Gly Leu Asn Thr Leu Thr Thr Tyr  
85 90 95

Val Pro Trp Asn Leu His Glu Pro Glu Arg Gly Lys Phe Asp Phe Ser  
           100                 105                 110

Gly Asn Leu Asp Leu Glu Ala Phe Val Leu Met Ala Ala Glu Ile Gly  
115 120 125

Leu Trp Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ser Glu Met Asp  
 130 135 140

Leu Gly Gly Leu Pro Ser Trp Leu Leu Gln Asp Pro Gly Met Arg Leu  
 145 150 155 160

Arg Thr Thr Tyr Lys Gly Phe Thr Glu Ala Val Asp Leu Tyr Phe Asp  
 165 170 175

His Leu Met Ser Arg Val Val Pro Leu Gln Tyr Lys Arg Gly Gly Pro  
 180 185 190

Ile Ile Ala Val Gln Val Glu Asn Glu Tyr Gly Ser Tyr Asn Lys Asp  
 195 200 205

Pro Ala Tyr Met Pro Tyr Val Lys Lys Ala Leu Glu Asp Arg Gly Ile  
 210 215 220

Val Glu Leu Leu Leu Thr Ser Asp Asn Lys Asp Gly Leu Ser Lys Gly  
 225 230 235 240

Ile Val Gln Gly Val Leu Ala Thr Ile Asn Leu Gln Ser Thr His Glu  
 245 250 255

Leu Gln Leu Leu Thr Thr Phe Leu Phe Asn Val Gln Gly Thr Gln Pro  
 260 265 270

Lys Met Val Met Glu Tyr Trp Thr Gly Trp Phe Asp Ser Trp Gly Gly  
 275 280 285

Pro His Asn Ile Leu Asp Ser Ser Glu Val Leu Lys Thr Val Ser Ala  
 290 295 300

Ile Val Asp Ala Gly Ser Ser Ile Asn Leu Tyr Met Phe His Gly Gly  
 305 310 315 320

Thr Asn Phe Gly Phe Met Asn Gly Ala Met His Phe His Asp Tyr Lys  
 325 330 335

Ser Asp Val Thr Ser Tyr Asp Tyr Asp Ala Val Leu Thr Glu Ala Gly  
 340 345 350

Asp Tyr Thr Ala Lys Tyr Met Lys Leu Arg Asp Phe Phe Gly Ser Ile  
 355 360 365

Ser Gly Ile Pro Leu Pro Pro Pro Asp Leu Leu Pro Lys Met Pro  
 370 375 380

Tyr Glu Pro Leu Thr Pro Val Leu Tyr Leu Ser Leu Trp Asp Ala Leu  
 385 390 395 400

Lys Tyr Leu Gly Glu Pro Ile Lys Ser Glu Lys Pro Ile Asn Met Glu  
 405 410 415

Asn Leu Pro Val Asn Gly Gly Asn Gly Gln Ser Phe Gly Tyr Ile Leu  
 420 425 430

Tyr Glu Thr Ser Ile Thr Ser Ser Gly Ile Leu Ser Gly His Val His  
 435 440 445

Asp Arg Gly Gln Val Phe Val Asn Thr Val Ser Ile Gly Phe Leu Asp  
 450 455 460

Tyr Lys Thr Thr Lys Ile Ala Val Pro Leu Ile Gln Gly Tyr Thr Val  
 465 470 475 480

Leu Arg Ile Leu Val Glu Asn Arg Gly Arg Val Asn Tyr Gly Glu Asn  
 485 490 495

Ile Asp Asp Gln Arg Lys Gly Leu Ile Gly Asn Leu Tyr Leu Asn Asp  
 500 505 510

Ser Pro Leu Lys Asn Phe Arg Ile Tyr Ser Leu Asp Met Lys Lys Ser  
 515 520 525

Phe Phe Gln Arg Phe Gly Leu Asp Lys Trp Xaa Ser Leu Pro Glu Thr  
 530 535 540

Pro Thr Leu Pro Ala Phe Phe Leu Gly Ser Leu Ser Ile Ser Ser Thr  
 545 550 555 560

Pro Cys Asp Thr Phe Leu Lys Leu Glu Gly Trp Glu Lys Gly Val Val  
 565 570 575

Phe Ile Asn Gly Gln Asn Leu Gly Arg Tyr Trp Asn Ile Gly Pro Gln  
 580 585 590

Lys Thr Leu Tyr Leu Pro Gly Pro Trp Leu Ser Ser Gly Ile Asn Gln  
 595 600 605

Val Ile Val Phe Glu Glu Thr Met Ala Gly Pro Ala Leu Gln Phe Thr  
 610 615 620

Glu Thr Pro His Leu Gly Arg Asn Gln Tyr Ile Lys  
 625 630 635

<210> 176

<211> 2505

<212> DNA

<213> Homo sapiens

<400> 176

ggggacgcgg agctgagagg ctccgggcta gctaggtgta ggggtggacg ggtcccagga 60  
 cccttgttag gtttctctac ttggccttcg gtgggggtca agacgcaggc acctacgc 120  
 aaggggagca aagccgggct cggcccgagg cccccaggac ctccatctcc caatgttgg 180  
 ggaatccgac acgtgacggt ctgtccgccc tctcagacta gaggagcgct gtaaaacgcca 240  
 tggctcccaa gaagctgtcc tgcttcgtt ccctgctgct gccgctcagc ctgacgctac 300  
 tgctccccca ggcagacact cggtcggtcg tagtgatag gggtcatgac cggttctcc 360  
 tagacggggc cccgttccgc tatgtgtctg gcagcctgca ctacttcgg gtaccgcggg 420

tgctttgggc cgaccggctt ttgaagatgc gatggagcgg cctcaacgcc atacagttt 480  
atgtgccctg gaactaccac gagccacagc ctggggtcta taacttaat ggcagccggg 540  
acctcattgc ctttctaat gaggcagtc tagcaaccc gttggtcata ctgagaccag 600  
gaccttacat ctgtcagag tggagatgg ggggtctccc atcctggttg cttcgaaaac 660  
ctgaaattca tctaagaacc tcagatccag acttccttgc cgcagtggac tcctggttca 720  
aggtcttgct gcccaagata tatccatggc ttatcacaa tggggcaac atcattagca 780  
ttcaggtgga gaatgaatat ggtagctaca gagcctgtga cttagctac atgaggcact 840  
tggctgggct ctccgtgca ctgcttaggag aaaagatctt gctctcacc acagatggc 900  
ctgaaggact caagtgtggc tccctccgg gactctatac cactgttagat ttggcccaag 960  
ctgacaacat gaccaaatac ttaccctgc ttcggaagta tgaacccat gggccattgg 1020  
taaactctga gtactacaca ggctggctgg attactgggg ccagaatcac tccacacgg 1080  
ctgtgtcagc tgtaaccaa ggactagaga acatgctaa gttggagcc agtgtgaaca 1140  
tgtacatgtt ccatggaggt accaacttg gatattggaa tggtggcgat aagaaggac 1200  
gcttccttcc gattactacc agctatgact atgatgcacc tatatctgaa gcaggggacc 1260  
ccacacctaa gcttttgc ctgcagatg toatcagcaa gttccaggaa ttcttttg 1320  
gaccttacc tcccccgagc cccaagatga tgcttgacc tgtgactctg cacctggttg 1380  
ggcatttact ggcttccta gacttgctt gccccgtgg gcccattcat tcaatcttc 1440  
caatgacctt tgaggctgca aagcaggacc atggcttcat gttgtaccga acctatatga 1500  
ccataccat ttttggcca acaccattct gggtgccaaa taatggagtc catgaccgtg 1560  
cctatgttat ggtggatggg gtgttccagg gtgttggaa gcaaataatg agagacaac 1620  
tatttttgac gggaaaactg gggtccaaac tggatatctt ggtggagaac atggggagac 1680  
tcagcttgg gtctaacagc agtgacttca agggcctgtt gaagccacca attctggggc 1740  
aaacaatcct taccctgtgg atgatgtcc ctctgaaaat tgataacctt gtgaagtgg 1800  
ggtttccctt ccagttgcca aaatggccat atcctcaagc tccttctggc cccacattt 1860  
actccaaaac atttccaatt ttaggctcg ttggggacac atttctatat ctacctggat 1920  
ggaccaaggg ccaagtctgg atcaatgggt ttaacttggg cggtaactgg acaaagcagg 1980  
ggccacaaca gaccctctac gtgccaagat tcctgctgtt tccttagggg gccctcaaca 2040  
aaattacatt gctggacta gaagatgtac ctctccagcc ccaagtccaa ttttggata 2100  
agcctatcct caatagcact agtacttgc acaggacaca tatcaattcc ctccagctg 2160  
atacactgag tgcctctgaa ccaatggagt taagtggga ctgaaaggta ggccgggcat 2220  
ggtggtcat gcctgtatc ccagcactt gggaggctga gacgggtggta ttacctgagg 2280  
tcaggactt aagaccagcc tggccaaat ggtgaaaccc cgtctccact aaaaatacaa 2340  
aaattagccg ggcgtgatgg tggccaccc taatcccagc tacttgggag gctgaggc 2400  
ggagaattgc ttgaatccag gaggcagagg ttgcagtggag tggaggtgt accactgcac 2460  
tccagcttgg ctgacagtga qacactccat ctcaaaaaaaa aaaaa 2505

<210> 177

<211> 654

<212> PRT

<213> Homo sapiens

<400> 177

Met Ala Pro Lys Lys Leu Ser Cys Leu Arg Ser Leu Leu Leu Pro Leu  
1 5 10 15

Ser Leu Thr Leu Leu Leu Pro Gln Ala Asp Thr Arg Ser Phe Val Val  
20 25 30

Asp Arg Gly His Asp Arg Phe Leu Leu Asp Gly Ala Pro Phe Arg Tyr  
35 40 45

Val Ser Gly Ser Leu His Tyr Phe Arg Val Pro Arg Val Leu Trp Ala  
50 55 60

Asp Arg Leu Leu Lys Met Arg Trp Ser Gly Leu Asn Ala Ile Gln Phe  
 65 70 75 80

Tyr Val Pro Trp Asn Tyr His Glu Pro Gln Pro Gly Val Tyr Asn Phe  
 85 90 95

Asn Gly Ser Arg Asp Leu Ile Ala Phe Leu Asn Glu Ala Ala Leu Ala  
 100 105 110

Asn Leu Leu Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ala Glu Trp  
 115 120 125

Glu Met Gly Gly Leu Pro Ser Trp Leu Leu Arg Lys Pro Glu Ile His  
 130 135 140

Leu Arg Thr Ser Asp Pro Asp Phe Leu Ala Ala Val Asp Ser Trp Phe  
 145 150 155 160

Lys Val Leu Leu Pro Lys Ile Tyr Pro Trp Leu Tyr His Asn Gly Gly  
 165 170 175

Asn Ile Ile Ser Ile Gln Val Glu Asn Glu Tyr Gly Ser Tyr Arg Ala  
 180 185 190

Cys Asp Phe Ser Tyr Met Arg His Leu Ala Gly Leu Phe Arg Ala Leu  
 195 200 205

Leu Gly Glu Lys Ile Leu Leu Phe Thr Thr Asp Gly Pro Glu Gly Leu  
 210 215 220

Lys Cys Gly Ser Leu Arg Gly Leu Tyr Thr Thr Val Asp Phe Gly Pro  
 225 230 235 240

Ala Asp Asn Met Thr Lys Ile Phe Thr Leu Leu Arg Lys Tyr Glu Pro  
 245 250 255

His Gly Pro Leu Val Asn Ser Glu Tyr Tyr Thr Gly Trp Leu Asp Tyr  
 260 265 270

Trp Gly Gln Asn His Ser Thr Arg Ser Val Ser Ala Val Thr Lys Gly  
 275 280 285

Leu Glu Asn Met Leu Lys Leu Gly Ala Ser Val Asn Met Tyr Met Phe  
 290 295 300

His Gly Gly Thr Asn Phe Gly Tyr Trp Asn Gly Ala Asp Lys Lys Gly  
 305 310 315 320

Arg Phe Leu Pro Ile Thr Thr Ser Tyr Asp Tyr Asp Ala Pro Ile Ser  
 325 330 335

Glu Ala Gly Asp Pro Thr Pro Lys Leu Phe Ala Leu Arg Asp Val Ile

340	345	350
Ser Lys Phe Gln Glu Val Pro Leu Gly Pro Leu Pro Pro Pro Ser Pro		
355	360	365
Lys Met Met Leu Gly Pro Val Thr Leu His Leu Val Gly His Leu Leu		
370	375	380
Ala Phe Leu Asp Leu Leu Cys Pro Arg Gly Pro Ile His Ser Ile Leu		
385	390	395 400
Pro Met Thr Phe Glu Ala Val Lys Gln Asp His Gly Phe Met Leu Tyr		
405	410	415
Arg Thr Tyr Met Thr His Thr Ile Phe Glu Pro Thr Pro Phe Trp Val		
420	425	430
Pro Asn Asn Gly Val His Asp Arg Ala Tyr Val Met Val Asp Gly Val		
435	440	445
Phe Gln Gly Val Val Glu Arg Asn Met Arg Asp Lys Leu Phe Leu Thr		
450	455	460
Gly Lys Leu Gly Ser Lys Leu Asp Ile Leu Val Glu Asn Met Gly Arg		
465	470	475 480
Leu Ser Phe Gly Ser Asn Ser Ser Asp Phe Lys Gly Leu Leu Lys Pro		
485	490	495
Pro Ile Leu Gly Gln Thr Ile Leu Thr Gln Trp Met Met Phe Pro Leu		
500	505	510
Lys Ile Asp Asn Leu Val Lys Trp Trp Phe Pro Leu Gln Leu Pro Lys		
515	520	525
Trp Pro Tyr Pro Gln Ala Pro Ser Gly Pro Thr Phe Tyr Ser Lys Thr		
530	535	540
Phe Pro Ile Leu Gly Ser Val Gly Asp Thr Phe Leu Tyr Leu Pro Gly		
545	550	555 560
Trp Thr Lys Gly Gln Val Trp Ile Asn Gly Phe Asn Leu Gly Arg Tyr		
565	570	575
Trp Thr Lys Gln Gly Pro Gln Gln Thr Leu Tyr Val Pro Arg Phe Leu		
580	585	590
Leu Phe Pro Arg Gly Ala Leu Asn Lys Ile Thr Leu Leu Glu Leu Glu		
595	600	605
Asp Val Pro Leu Gln Pro Gln Val Gln Phe Leu Asp Lys Pro Ile Leu		
610	615	620

Asn Ser Thr Ser Thr Leu His Arg Thr His Ile Asn Ser Leu Ser Ala  
 625 630 635 640

Asp Thr Leu Ser Ala Ser Glu Pro Met Glu Leu Ser Gly His  
 645 650

<210> 178

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 178

tggctactcc aagaccctgg catg

24

<210> 179

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 179

tggacaaaatc cccttgctca gccc

24

<210> 180

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 180

gggcattcacc gaaggcagtgg acctttatcc tgaccacctg atgtccaggg

50

<210> 181

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 181

ccagctatga ctatgatgca cc

22

<210> 182  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 182  
tggcacccag aatggtgttg gctc 24

<210> 183  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 183  
cgagatgtca tcagcaagtt ccaggaagtt cctttggac ctttacctcc 50

<210> 184  
<211> 1947  
<212> DNA  
<213> Homo sapiens

<400> 184  
gctttgaaca cgtctgcaag cccaaagttg agcatctgat tggtagatgg gtatttgagt 60  
gcaccaccaa tatggcttac atgtaaaaaa agcttctcat cagttacata tccattattt 120  
gtgttatgg ctatctgc ctctacactc tcttctggtt attcaggata ccttgaagg 180  
aatattctt cggaaaagtc agagaagaga gcagtttag tgacattcca gatgtcaaaa 240  
acgattttgc gtccttctt cacatggtag accagttatga ccagctatat tccaagcggt 300  
ttggtggtt ctgtcagaa gttagtgaaa ataaacttag ggaaatttagt ttgaaccatg 360  
agtggacatt tgaaaaactc aggacgaca tttcacgcaa cgcccaggac aacgcaggagt 420  
tgcattgtt catgtgtcg ggggtccccg atgctgtt tgacctcaca gacctggatg 480  
tgctaaagct tgaactaatt ccagaagcta aaattctgc taagattct caaatgacta 540  
acctccaaaga gtcacccctc tgccactgcc ctgcaaaagt tgaacagact gcttttagct 600  
ttcttcgcga tcaacttgaga tgccttcacg tgaagttcac ttagtggct qaaattcctg 660  
cctgggtgta ttgctcaaa aaccttcgag agttgtactt aataggcaat ttgaactctg 720  
aaaacaataa gatgatagga cttgaatctc tccgagagtt gcggcacctt aagattctcc 780  
acgtgaagag caatttgacc aaagttccct ccaacattac agatgtggct ccacatctta 840  
caaagtttagt cattcataat gacggcacta aactcttggt actgaacagc cttaaagaaaa 900  
ttagtgaatgt cgctgagctg gaactccaga actgtgagct agagagaatc ccacatgcta 960  
ttttcagcct ctctaattta caggaactgg atttaaagtca aataaacatt cgcacaattg 1020  
aggaaatcat cagttccag cattttaaac gactgacttg tttaaaatta tggcataaca 1080  
aaattgttac tattcctccc tctattaccc atgtcaaaaaa cttggagtca ctttatttct 1140  
ctaacaacaa gctcgaatcc ttaccagtgg cagttatgg tttacagaaa ctcagatgct 1200  
tagatgtgag ctacaacaac attcaatga ttccaaataga aataggattg cttcagaacc 1260  
tgcagcattt gcataatcact gggaaacaaag tggacattct gccaaaacaa ttgtttaat 1320

gcataaagtt gaggacttg aatctggac agaactgcat cacctcactc ccagagaaaag 1380  
 ttggtcagct ctcccagtc actcagctgg agctgaaggg gaactgctt gaccgcctgc 1440  
 cagcccagct gggccagtgt cgatgctca agaaaagcgg gcttgttggta gaagatcacc 1500  
 ttttgatac cctgccactc gaagtcaaag aggcatgaa tcaagacata aatattccct 1560  
 ttgcaaatgg gattttaact aagataatat atgcacagtg atgtgcagga acaacttcct 1620  
 agattgcaag tgctcacgta caagttatta caagataatg catttttagga gtagatacat 1680  
 cttttaaat aaaacagaga ggatgcatag aaggctgata gaagacataa ctgaatgttc 1740  
 aatgtttgta gggtttaag tcattcattt ccaaattcatt ttttttttc ttttgggaa 1800  
 agggaggaa aaattataat cactaatctt gttctttt aaattgtttg taactggat 1860  
 gctgccgcta ctgaatgtt acaaattgct tgcctgctaa agtaaatgat taaattgaca 1920  
 ttttctact aaaaaaaaaaaaaaa 1947

&lt;210&gt; 185

&lt;211&gt; 501

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 185

Met	Ala	Tyr	Met	Leu	Lys	Lys	Leu	Leu	Ile	Ser	Tyr	Ile	Ser	Ile	Ile
1				5				10					15		

Cys	Val	Tyr	Gly	Phe	Ile	Cys	Leu	Tyr	Thr	Leu	Phe	Trp	Leu	Phe	Arg
					20				25				30		

Ile	Pro	Leu	Lys	Glu	Tyr	Ser	Phe	Glu	Lys	Val	Arg	Glu	Glu	Ser	Ser
					35			40				45			

Phe	Ser	Asp	Ile	Pro	Asp	Val	Lys	Asn	Asp	Phe	Ala	Phe	Leu	Leu	His
					50			55			60				

Met	Val	Asp	Gln	Tyr	Asp	Gln	Leu	Tyr	Ser	Lys	Arg	Phe	Gly	Val	Phe
					65			70			75		80		

Leu	Ser	Glu	Val	Ser	Glu	Asn	Lys	Leu	Arg	Glu	Ile	Ser	Leu	Asn	His
					85				90			95			

Glu	Trp	Thr	Phe	Glu	Lys	Leu	Arg	Gln	His	Ile	Ser	Arg	Asn	Ala	Gln
					100			105			110				

Asp	Lys	Gln	Glu	Leu	His	Leu	Phe	Met	Leu	Ser	Gly	Val	Pro	Asp	Ala
					115			120			125				

Val	Phe	Asp	Leu	Thr	Asp	Leu	Asp	Val	Leu	Lys	Leu	Glu	Leu	Ile	Pro
					130			135			140				

Glu	Ala	Lys	Ile	Pro	Ala	Lys	Ile	Ser	Gln	Met	Thr	Asn	Leu	Gln	Glu
					145			150			155		160		

Leu	His	Leu	Cys	His	Cys	Pro	Ala	Lys	Val	Glu	Gln	Thr	Ala	Phe	Ser
					165			170			175				

Phe	Leu	Arg	Asp	His	Leu	Arg	Cys	Leu	His	Val	Lys	Phe	Thr	Asp	Val
					180			185			190				

Ala Glu Ile Pro Ala Trp Val Tyr Leu Leu Lys Asn Leu Arg Glu Leu  
 195 200 205

Tyr Leu Ile Gly Asn Leu Asn Ser Glu Asn Asn Lys Met Ile Gly Leu  
 210 215 220

Glu Ser Leu Arg Glu Leu Arg His Leu Lys Ile Leu His Val Lys Ser  
 225 230 235 240

Asn Leu Thr Lys Val Pro Ser Asn Ile Thr Asp Val Ala Pro His Leu  
 245 250 255

Thr Lys Leu Val Ile His Asn Asp Gly Thr Lys Leu Leu Val Leu Asn  
 260 265 270

Ser Leu Lys Lys Met Met Asn Val Ala Glu Leu Glu Leu Gln Asn Cys  
 275 280 285

Glu Leu Glu Arg Ile Pro His Ala Ile Phe Ser Leu Ser Asn Leu Gln  
 290 295 300

Glu Leu Asp Leu Lys Ser Asn Asn Ile Arg Thr Ile Glu Glu Ile Ile  
 305 310 315 320

Ser Phe Gln His Leu Lys Arg Leu Thr Cys Leu Lys Leu Trp His Asn  
 325 330 335

Lys Ile Val Thr Ile Pro Pro Ser Ile Thr His Val Lys Asn Leu Glu  
 340 345 350

Ser Leu Tyr Phe Ser Asn Asn Lys Leu Glu Ser Leu Pro Val Ala Val  
 355 360 365

Phe Ser Leu Gln Lys Leu Arg Cys Leu Asp Val Ser Tyr Asn Asn Ile  
 370 375 380

Ser Met Ile Pro Ile Glu Ile Gly Leu Leu Gln Asn Leu Gln His Leu  
 385 390 395 400

His Ile Thr Gly Asn Lys Val Asp Ile Leu Pro Lys Gln Leu Phe Lys  
 405 410 415

Cys Ile Lys Leu Arg Thr Leu Asn Leu Gly Gln Asn Cys Ile Thr Ser  
 420 425 430

Leu Pro Glu Lys Val Gly Gln Leu Ser Gln Leu Thr Gln Leu Glu Leu  
 435 440 445

Lys Gly Asn Cys Leu Asp Arg Leu Pro Ala Gln Leu Gly Gln Cys Arg  
 450 455 460

Met Leu Lys Lys Ser Gly Leu Val Val Glu Asp His Leu Phe Asp Thr

465 470 475 480

Leu Pro Leu Glu Val Lys Glu Ala Leu Asn Gln Asp Ile Asn Ile Pro  
485 490 495

Phe Ala Asn Gly Ile  
500

<210> 186  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 186  
cctccctcta ttacccatgt c 21

<210> 187  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 187  
gaccaacttt ctctggag gagg 24

<210> 188  
<211> 47  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 188  
gtcactttat ttctctaaca acaagctcg atccttacca gtggcag 47

<210> 189  
<211> 2917  
<212> DNA  
<213> Homo sapiens

<400> 189  
ccccacgcgtc cggccttctc tctggacttt gcatttccat tcctttcat tgacaaaactg 60  
actttttta ttttttttt tccatctctg ggccagcttg ggatccttagg ccgccttggg 120  
aagacatttg tggtttacac acataaggat ctgtgtttgg ggtttcttct tcttcccctg 180

<210> 190  
<211> 607  
<212> PRT  
<213> *Homo sapiens*

<400> 190

Met Glu Leu Val Arg Arg Leu Met Pro Leu Thr Leu Leu Ile Leu Ser  
 1 5 10 15

Cys Leu Ala Glu Leu Thr Met Ala Glu Ala Glu Gly Asn Ala Ser Cys  
 20 25 30

Thr Val Ser Leu Gly Gly Ala Asn Met Ala Glu Thr His Lys Ala Met  
 35 40 45

Ile Leu Gln Leu Asn Pro Ser Glu Asn Cys Thr Trp Thr Ile Glu Arg  
 50 55 60

Pro Glu Asn Lys Ser Ile Arg Ile Ile Phe Ser Tyr Val Gln Leu Asp  
 65 70 75 80

Pro Asp Gly Ser Cys Glu Ser Glu Asn Ile Lys Val Phe Asp Gly Thr  
 85 90 95

Ser Ser Asn Gly Pro Leu Leu Gly Gln Val Cys Ser Lys Asn Asp Tyr  
 100 105 110

Val Pro Val Phe Glu Ser Ser Ser Thr Leu Thr Phe Gln Ile Val  
 115 120 125

Thr Asp Ser Ala Arg Ile Gln Arg Thr Val Phe Val Phe Tyr Tyr Phe  
 130 135 140

Phe Ser Pro Asn Ile Ser Ile Pro Asn Cys Gly Gly Tyr Leu Asp Thr  
 145 150 155 160

Leu Glu Gly Ser Phe Thr Ser Pro Asn Tyr Pro Lys Pro His Pro Glu  
 165 170 175

Leu Ala Tyr Cys Val Trp His Ile Gln Val Glu Lys Asp Tyr Lys Ile  
 180 185 190

Lys Leu Asn Phe Lys Glu Ile Phe Leu Glu Ile Asp Lys Gln Cys Lys  
 195 200 205

Phe Asp Phe Leu Ala Ile Tyr Asp Gly Pro Ser Thr Asn Ser Gly Leu  
 210 215 220

Ile Gly Gln Val Cys Gly Arg Val Thr Pro Thr Phe Glu Ser Ser Ser  
 225 230 235 240

Asn Ser Leu Thr Val Val Leu Ser Thr Asp Tyr Ala Asn Ser Tyr Arg  
 245 250 255

Gly Phe Ser Ala Ser Tyr Thr Ser Ile Tyr Ala Glu Asn Ile Asn Thr  
 260 265 270

Thr Ser Leu Thr Cys Ser Ser Asp Arg Met Arg Val Ile Ile Ser Lys  
 275 280 285

Ser Tyr Leu Glu Ala Phe Asn Ser Asn Gly Asn Asn Leu Gln Leu Lys  
 290 295 300

Asp Pro Thr Cys Arg Pro Lys Leu Ser Asn Val Val Glu Phe Ser Val  
 305 310 315 320

Pro Leu Asn Gly Cys Gly Thr Ile Arg Lys Val Glu Asp Gln Ser Ile  
 325 330 335

Thr Tyr Thr Asn Ile Ile Thr Phe Ser Ala Ser Ser Thr Ser Glu Val  
 340 345 350

Ile Thr Arg Gln Lys Gln Leu Gln Ile Ile Val Lys Cys Glu Met Gly  
 355 360 365

His Asn Ser Thr Val Glu Ile Ile Tyr Ile Thr Glu Asp Asp Val Ile  
 370 375 380

Gln Ser Gln Asn Ala Leu Gly Lys Tyr Asn Thr Ser Met Ala Leu Phe  
 385 390 395 400

Glu Ser Asn Ser Phe Glu Lys Thr Ile Leu Glu Ser Pro Tyr Tyr Val  
 405 410 415

Asp Leu Asn Gln Thr Leu Phe Val Gln Val Ser Leu His Thr Ser Asp  
 420 425 430

Pro Asn Leu Val Val Phe Leu Asp Thr Cys Arg Ala Ser Pro Thr Ser  
 435 440 445

Asp Phe Ala Ser Pro Thr Tyr Asp Leu Ile Lys Ser Gly Cys Ser Arg  
 450 455 460

Asp Glu Thr Cys Lys Val Tyr Pro Leu Phe Gly His Tyr Gly Arg Phe  
 465 470 475 480

Gln Phe Asn Ala Phe Lys Phe Leu Arg Ser Met Ser Ser Val Tyr Leu  
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Gln Cys Lys Val Leu Ile Cys Asp Ser Ser Asp His Gln Ser Arg Cys  
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Asn Gln Gly Cys Val Ser Arg Ser Lys Arg Asp Ile Ser Ser Tyr Lys  
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Trp Lys Thr Asp Ser Ile Ile Gly Pro Ile Arg Leu Lys Arg Asp Arg  
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Ser Ala Ser Gly Asn Ser Gly Phe Gln His Glu Thr His Ala Glu Glu  
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Thr Pro Asn Gln Pro Phe Asn Ser Val His Leu Phe Ser Phe Met Val

565

570

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Arg	Phe	Asp	Pro	Thr	Trp	Glu	Ser	Leu	Asp	Ala	Arg	Gln	Leu	Pro	Ala
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Ile Val Leu Thr Ser Lys His His Glu Gly Phe Thr Leu Trp Gly Ser  
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Phe Gly Leu Tyr Tyr Ser Leu Phe Glu Trp Phe His Pro Leu Phe Leu  
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Glu Asp Glu Ser Ser Ser Phe His Lys Arg Gln Phe Pro Val Ser Lys  
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Leu Trp Ser Asp Gly Asp Gly Ala Pro Asp Gln Tyr Trp Asn Ser  
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Val Val Thr Asn Asp Arg Trp Gly Ala Gly Ser Ile Cys Lys His Gly  
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Gly Phe Tyr Thr Cys Ser Asp Arg Tyr Asn Pro Gly His Leu Leu Pro  
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His Lys Trp Glu Asn Cys Met Thr Ile Asp Lys Leu Ser Trp Gly Tyr  
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Arg Arg Glu Ala Gly Ile Ser Asp Tyr Leu Thr Ile Glu Glu Leu Val  
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Lys Gln Leu Val Glu Thr Val Ser Cys Gly Gly Asn Leu Leu Met Asn  
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PDB ID: 2D9C

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Glu Thr Tyr Thr Trp Arg Ser Gln Asn Asp Thr Val Thr Pro Asp Val  
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Lys Trp Pro Thr Ser Gly Gln Leu Phe Leu Gly His Pro Lys Ala Ile  
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Leu Gly Ala Thr Glu Val Lys Leu Leu Gly His Gly Gln Pro Leu Asn  
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Trp Ile Ser Leu Glu Gln Asn Gly Ile Met Val Glu Leu Pro Gln Leu  
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Asn Val Ile  
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&lt;210&gt; 201

&lt;211&gt; 322

&lt;212&gt; PRT

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; Synthetic protein

&lt;400&gt; 201

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Thr	Arg	Leu	Leu	Val	Gln	Gly	Ser	Leu	Arg	Ala	Glu	Glu	Leu	Ser	Ile
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Gln	Val	Ser	Cys	Arg	Ile	Met	Gly	Ile	Thr	Leu	Val	Ser	Lys	Lys	Ala
					35			40					45		

Asn	Gln	Gln	Leu	Asn	Phe	Thr	Glu	Ala	Lys	Glu	Ala	Cys	Arg	Leu	Leu
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Gly	Leu	Ser	Leu	Ala	Gly	Lys	Asp	Gln	Val	Glu	Thr	Ala	Leu	Lys	Ala
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Ser	Phe	Glu	Thr	Cys	Ser	Tyr	Gly	Trp	Val	Gly	Asp	Gly	Phe	Val	Val
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Ile	Ser	Arg	Ile	Ser	Pro	Asn	Pro	Lys	Cys	Gly	Lys	Asn	Gly	Val	Gly
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Val	Leu	Ile	Trp	Lys	Val	Pro	Val	Ser	Arg	Gln	Phe	Ala	Ala	Tyr	Cys
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Tyr	Asn	Ser	Ser	Asp	Thr	Trp	Thr	Asn	Ser	Cys	Ile	Pro	Glu	Ile	Ile
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Thr Thr Lys Asp Pro Ile Phe Asn Thr Gln Thr Ala Thr Gln Thr Thr  
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 Thr Ser Thr Met Ser Thr Glu Thr Glu Pro Phe Val Glu Asn Lys Ala  
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 <210> 203  
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 <213> Artificial Sequence

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<220>
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<210> 205
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<223> a, t, c or g

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<211> 296

<212> PRT

<213> Homo sapiens

<400> 207

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Leu Pro Thr Gln Arg Glu Asp Gly Asn Pro Cys Asp Phe Asp Trp Arg  
50 55 60

Glu Val Glu Ile Leu Met Phe Leu Ser Ala Ile Val Met Met Lys Asn  
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Arg Arg Ser Ile Thr Val Glu Gln His Ile Gly Asn Ile Phe Met Phe  
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Ser Lys Val Ala Asn Thr Ile Leu Phe Phe Arg Leu Asp Ile Arg Met  
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Gly Leu Leu Tyr Ile Thr Leu Cys Ile Val Phe Leu Met Thr Cys Lys  
 115 120 125

Pro Pro Leu Tyr Met Gly Pro Glu Tyr Ile Lys Tyr Phe Asn Asp Lys  
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Thr Ile Asp Glu Glu Leu Glu Arg Asp Lys Arg Val Thr Trp Ile Val  
 145 150 155 160

Glu Phe Phe Ala Asn Trp Ser Asn Asp Cys Gln Ser Phe Ala Pro Ile  
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Tyr Ala Asp Leu Ser Leu Lys Tyr Asn Cys Thr Gly Leu Asn Phe Gly  
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Lys Val Asp Val Gly Arg Tyr Thr Asp Val Ser Thr Arg Tyr Lys Val  
 195 200 205

Ser Thr Ser Pro Leu Thr Lys Gln Leu Pro Thr Leu Ile Leu Phe Gln  
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Gly Gly Lys Glu Ala Met Arg Arg Pro Gln Ile Asp Lys Lys Gly Arg  
 225 230 235 240

Ala Val Ser Trp Thr Phe Ser Glu Glu Asn Val Ile Arg Glu Phe Asn  
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Leu Asn Glu Leu Tyr Gln Arg Ala Lys Lys Leu Ser Lys Ala Gly Asp  
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Asn Ile Pro Glu Glu Gln Pro Val Ala Ser Thr Pro Thr Thr Val Ser  
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<210> 208

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<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

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<210> 210  
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 <212> DNA  
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<210> 213

<211> 360

<212> PBT

<213> Homo sapiens

<400> 213

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20 25 30

Gln Asn Leu Gly Asn Gly His Gly Lys Asp Leu Leu Asn Gly Val Lys  
35 40 45

Leu Val Val Glu Thr Pro Glu Glu Thr Leu Phe Thr Tyr Gln Gly Ala  
50 55 60

Ser Val Ile Leu Pro Cys Arg Tyr Arg Tyr Glu Pro Ala Leu Val Ser  
65 70 75 80

Pro Arg Arg Val Arg Val Lys Trp Trp Lys Leu Ser Glu Asn Gly Ala  
85 90 95

Pro Glu Lys Asp Val Leu Val Ala Ile Gly Leu Arg His Arg Ser Phe  
           100                 105                 110

Gly Asp Tyr Gln Gly Arg Val His Leu Arg Gln Asp Lys Glu His Asp

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Arg Cys Glu Val Ile Asp Gly Leu Glu Asp Glu Ser Gly Leu Val Glu		
145	150	155
Leu Glu Leu Arg Gly Val Val Phe Pro Tyr Gln Ser Pro Asn Gly Arg		
165	170	175
Tyr Gln Phe Asn Phe His Glu Gly Gln Gln Val Cys Ala Glu Gln Ala		
180	185	190
Ala Val Val Ala Ser Phe Glu Gln Leu Phe Arg Ala Trp Glu Glu Gly		
195	200	205
Leu Asp Trp Cys Asn Ala Gly Trp Leu Gln Asp Ala Thr Val Gln Tyr		
210	215	220
Pro Ile Met Leu Pro Arg Gln Pro Cys Gly Gly Pro Gly Leu Ala Pro		
225	230	235
Gly Val Arg Ser Tyr Gly Pro Arg His Arg Arg Leu His Arg Tyr Asp		
245	250	255
Val Phe Cys Phe Ala Thr Ala Leu Lys Gly Arg Val Tyr Tyr Leu Glu		
260	265	270
His Pro Glu Lys Leu Thr Leu Thr Glu Ala Arg Glu Ala Cys Gln Glu		
275	280	285
Asp Asp Ala Thr Ile Ala Lys Val Gly Gln Leu Phe Ala Ala Trp Lys		
290	295	300
Phe His Gly Leu Asp Arg Cys Asp Ala Gly Trp Leu Ala Asp Gly Ser		
305	310	315
Val Arg Tyr Pro Val Val His Pro His Pro Asn Cys Gly Pro Pro Glu		
325	330	335
Pro Gly Val Arg Ser Phe Gly Phe Pro Asp Pro Gln Ser Arg Leu Tyr		
340	345	350
Gly Val Tyr Cys Tyr Arg Gln His		
355	360	

&lt;210&gt; 214

&lt;211&gt; 18

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 214  
tgcttcgcta ctgccctc

18

<210> 215  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 215  
ttcccttgtg ggttggag

18

<210> 216  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 216  
agggctggaa gccagttc

18

<210> 217  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 217  
agccagttag gaaatgcg

18

<210> 218  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 218  
tgtccaaagt acacacacct gagg

24

<210> 219  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 219  
 gatgccacga tcgccaagg gggacagctc tttgccgcct ggaag 45

<210> 220  
 <211> 1503  
 <212> DNA  
 <213> Homo sapiens

<400> 220  
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 tggccagggg agggtgcacc aggccggccc cctgagcgac gctccccatg atgacgcccc 180  
 cgggaacttc cagtagcacc atgaggctt cctgggacgg gaagtggcca aggaattcga 240  
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 aaa 1503

<210> 221  
 <211> 328  
 <212> PRT  
 <213> Homo sapiens

<400> 221  
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Arg	Val	His	Gln	Ala	Ala	Pro	Leu	Ser	Asp	Ala	Pro	His	Asp	Asp	Ala	
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His	Gly	Asn	Phe	Gln	Tyr	Asp	His	Glu	Ala	Phe	Leu	Gly	Arg	Glu	Val	
					50			55				60				
Ala	Lys	Glu	Phe	Asp	Gln	Leu	Thr	Pro	Glu	Glu	Ser	Gln	Ala	Arg	Leu	
					65			70			75			80		
Gly	Arg	Ile	Val	Asp	Arg	Met	Asp	Arg	Ala	Gly	Asp	Gly	Asp	Gly	Trp	
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Val	Ser	Leu	Ala	Glu	Leu	Arg	Ala	Trp	Ile	Ala	His	Thr	Gln	Gln	Arg	
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His	Ile	Arg	Asp	Ser	Val	Ser	Ala	Ala	Trp	Asp	Thr	Tyr	Asp	Thr	Asp	
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Arg	Asp	Gly	Arg	Val	Gly	Trp	Glu	Glu	Leu	Arg	Asn	Ala	Thr	Tyr	Gly	
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His	Tyr	Ala	Pro	Gly	Glu	Glu	Phe	His	Asp	Val	Glu	Asp	Ala	Glu	Thr	
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Tyr	Lys	Lys	Met	Leu	Ala	Arg	Asp	Glu	Arg	Arg	Phe	Arg	Val	Ala	Asp	
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Gln	Asp	Gly	Asp	Ser	Met	Ala	Thr	Arg	Glu	Glu	Leu	Thr	Ala	Phe	Leu	
					180				185					190		
His	Pro	Glu	Glu	Phe	Pro	His	Met	Arg	Asp	Ile	Val	Ile	Ala	Glu	Thr	
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Leu	Glu	Asp	Leu	Asp	Arg	Asn	Lys	Asp	Gly	Tyr	Val	Gln	Val	Glu	Glu	
					210			215			220					
Tyr	Ile	Ala	Asp	Leu	Tyr	Ser	Ala	Glu	Pro	Gly	Glu	Glu	Pro	Ala		
					225				230			235			240	
Trp	Val	Gln	Thr	Glu	Arg	Gln	Gln	Phe	Arg	Asp	Phe	Arg	Asp	Leu	Asn	
					245				250					255		
Lys	Asp	Gly	His	Leu	Asp	Gly	Ser	Glu	Val	Gly	His	Trp	Val	Leu	Pro	
					260				265					270		
Pro	Ala	Gln	Asp	Gln	Pro	Leu	Val	Glu	Ala	Asn	His	Leu	Leu	His	Glu	
					275				280					285		

Ser Asp Thr Asp Lys Asp Gly Arg Leu Ser Lys Ala Glu Ile Leu Gly  
290 295 300

Asn Trp Asn Met Phe Val Gly Ser Gln Ala Thr Asn Tyr Gly Glu Asp  
 305                   310                   315                   320

Leu Thr Arg His His Asp Glu Leu  
325

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<210> 222  
<211> 20  
<212> DNA  
<213> Artificial Sequence
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<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 222  
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<210> 223  
<211> 18  
<212> DNA  
<213> Artificial Sequence
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<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 223  
gaaatccctgg gtaattgg 18

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<210> 224
<211> 23
<212> DNA
<213> Artificial Sequence
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<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 224  
gtgcgcggtg ctcacagctc atc 23

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<210> 225
<211> 44
<212> DNA
<213> Artificial Sequence
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<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 225  
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 <210> 226  
 <211> 2403  
 <212> DNA  
 <213> Homo sapiens  
  
 <400> 226  
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 aaa 2403

<210> 227

<211> 550  
<212> PRT  
<213> Homo sapiens

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Thr Cys Phe Thr Arg Gly Leu Asp Ile Arg Lys Glu Lys Ala Asp Val  
35 40 45  
Leu Cys Pro Gly Gly Cys Pro Leu Glu Glu Phe Ser Val Tyr Gly Asn  
50 55 60  
Ile Val Tyr Ala Ser Val Ser Ser Ile Cys Gly Ala Ala Val His Arg  
65 70 75 80  
Gly Val Ile Ser Asn Ser Gly Gly Pro Val Arg Val Tyr Ser Leu Pro  
85 90 95  
Gly Arg Glu Asn Tyr Ser Ser Val Asp Ala Asn Gly Ile Gln Ser Gln  
100 105 110  
Met Leu Ser Arg Trp Ser Ala Ser Phe Thr Val Thr Lys Gly Lys Ser  
115 120 125  
Ser Thr Gln Glu Ala Thr Gly Gln Ala Val Ser Thr Ala His Pro Pro  
130 135 140  
Thr Gly Lys Arg Leu Lys Lys Thr Pro Glu Lys Lys Thr Gly Asn Lys  
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Asp Cys Lys Ala Asp Ile Ala Phe Leu Ile Asp Gly Ser Phe Asn Ile  
165 170 175  
Gly Gln Arg Arg Phe Asn Leu Gln Lys Asn Phe Val Gly Lys Val Ala  
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Leu Met Leu Gly Ile Gly Thr Glu Gly Pro His Val Gly Leu Val Gln  
195 200 205  
Ala Ser Glu His Pro Lys Ile Glu Phe Tyr Leu Lys Asn Phe Thr Ser  
210 215 220  
Ala Lys Asp Val Leu Phe Ala Ile Lys Glu Val Gly Phe Arg Gly Gly  
225 230 235 240  
Asn Ser Asn Thr Gly Lys Ala Leu Lys His Thr Ala Gln Lys Phe Phe  
245 250 255

Thr Val Asp Ala Gly Val Arg Lys Gly Ile Pro Lys Val Val Val  
 260 265 270

Phe Ile Asp Gly Trp Pro Ser Asp Asp Ile Glu Glu Ala Gly Ile Val  
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Ala Arg Glu Phe Gly Val Asn Val Phe Ile Val Ser Val Ala Lys Pro  
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Ile Pro Glu Glu Leu Gly Met Val Gln Asp Val Thr Phe Val Asp Lys  
 305 310 315 320

Ala Val Cys Arg Asn Asn Gly Phe Phe Ser Tyr His Met Pro Asn Trp  
 325 330 335

Phe Gly Thr Thr Lys Tyr Val Lys Pro Leu Val Gln Lys Leu Cys Thr  
 340 345 350

His Glu Gln Met Met Cys Ser Lys Thr Cys Tyr Asn Ser Val Asn Ile  
 355 360 365

Ala Phe Leu Ile Asp Gly Ser Ser Ser Val Gly Asp Ser Asn Phe Arg  
 370 375 380

Leu Met Leu Glu Phe Val Ser Asn Ile Ala Lys Thr Phe Glu Ile Ser  
 385 390 395 400

Asp Ile Gly Ala Lys Ile Ala Ala Val Gln Phe Thr Tyr Asp Gln Arg  
 405 410 415

Thr Glu Phe Ser Phe Thr Asp Tyr Ser Thr Lys Glu Asn Val Leu Ala  
 420 425 430

Val Ile Arg Asn Ile Arg Tyr Met Ser Gly Gly Thr Ala Thr Gly Asp  
 435 440 445

Ala Ile Ser Phe Thr Val Arg Asn Val Phe Gly Pro Ile Arg Glu Ser  
 450 455 460

Pro Asn Lys Asn Phe Leu Val Ile Val Thr Asp Gly Gln Ser Tyr Asp  
 465 470 475 480

Asp Val Gln Gly Pro Ala Ala Ala His Asp Ala Gly Ile Thr Ile  
 485 490 495

Phe Ser Val Gly Val Ala Trp Ala Pro Leu Asp Asp Leu Lys Asp Met  
 500 505 510

Ala Ser Lys Pro Lys Glu Ser His Ala Phe Phe Thr Arg Glu Phe Thr  
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Phe Leu Glu Ser Gln Gln  
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<210> 228  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 228  
tggtctcgca caccgatc 18

<210> 229  
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<212> DNA  
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oligonucleotide probe

<400> 229  
ctgctgtcca caggggag 18

<210> 230  
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<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 230  
ccttgaagca tactgctc 18

<210> 231  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 231  
gagatagcaa tttccgccc 18

<210> 232

<211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 232  
 ttcctcaaga gggcagcc 18

<210> 233  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 233  
 cttggcacca atgtccgaga ttcc 24

<210> 234  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 234  
 gctctgagga aggtgacgcg cggggcctcc gaacccttgg ccttg 45

<210> 235  
 <211> 2586  
 <212> DNA  
 <213> Homo sapiens

<400> 235  
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 gtccggggcg 180  
 gcctgtgtgt 240  
 ctccagtcaa 300  
 tgttccgcga 360  
 aagagatgga 420  
 tacctcccag 480  
 atgtgcaccc 540  
 agacagttat 600  
 acgaggactg 660  
 catgccgggg 720  
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&lt;210&gt; 236

&lt;211&gt; 350

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 236

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5

10

15

Val	Pro	Thr	Ala	Pro	Ala	Pro	Ala	Pro	Thr	Ala	Thr	Ser	Ala	Pro	Val
20															

25

30

Lys	Pro	Gly	Pro	Ala	Leu	Ser	Tyr	Pro	Gln	Glu	Glu	Ala	Thr	Leu	Asn
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35

40

45

Glu	Met	Phe	Arg	Glu	Val	Glu	Glu	Leu	Met	Glu	Asp	Thr	Gln	His	Lys
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55

60

Leu	Arg	Ser	Ala	Val	Glu	Glu	Met	Glu	Ala	Glu	Glu	Ala	Ala	Lys
65														

70

75

80

Ala Ser Ser Glu Val Asn Leu Ala Asn Leu Pro Pro Ser Tyr His Asn  
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                   165                 170                     175  
  
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 Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu  
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 Cys His Asp Pro Ala Ser Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu  
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 Cys Gln Pro His Ser His Ser Leu Val Tyr Val Cys Lys Pro Thr Phe  
                   275                 280                     285  
  
 Val Gly Ser Arg Asp Gln Asp Gly Glu Ile Leu Leu Pro Arg Glu Val  
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 Pro Asp Glu Tyr Glu Val Gly Ser Phe Met Glu Glu Val Arg Gln Glu  
                   305                 310                     315                     320  
  
 Leu Glu Asp Leu Glu Arg Ser Leu Thr Glu Glu Met Ala Leu Gly Glu  
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<210> 243  
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<210> 244  
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<213> Homo Sapien

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<211> 713

<212> PRT

<213> Homo Sapien

<400> 245

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35 40 45

Ser Tyr Arg Glu Ala Thr Thr Val Asp Cys Asn Asp Leu Phe Leu  
50 55 60

Thr Ala Val Pro Pro Ala Leu Pro Ala Gly Thr Gln Thr Leu Leu  
65 70 75

Leu Gln Ser Asn Ser Ile Val Arg Val Asp Gln Ser Glu Leu Gly  
80 85 90

Tyr Leu Ala Asn Leu Thr Glu Leu Asp Leu Ser Gln Asn Ser Phe  
95 100 105

Ser Asp Ala Arg Asp Cys Asp Phe His Ala Leu Pro Gln Leu Leu  
110 115 120

Ser Phe Ala Gly Leu Ala Ser Leu Gln Glu Leu Tyr Leu Asn His  
140 145 150

Asn Gln Leu Tyr Arg Ile Ala Pro Arg Ala Phe Ser Gly Leu Ser  
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 Asp Ser Arg Trp Phe Glu Met Leu Pro Asn Leu Glu Ile Leu Met  
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 Ile Gly Gly Asn Lys Val Asp Ala Ile Leu Asp Met Asn Phe Arg  
                  200                     205                 210  
  
 Pro Leu Ala Asn Leu Arg Ser Leu Val Leu Ala Gly Met Asn Leu  
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                  260                     265                 270  
  
 Asn Pro Leu Gln Arg Val Gly Pro Gly Asp Phe Ala Asn Met Leu  
                  275                     280                 285  
  
 His Leu Lys Glu Leu Gly Leu Asn Asn Met Glu Glu Leu Val Ser  
                  290                     295                 300  
  
 Ile Asp Lys Phe Ala Leu Val Asn Leu Pro Glu Leu Thr Lys Leu  
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 Asp Ile Thr Asn Asn Pro Arg Leu Ser Phe Ile His Pro Arg Ala  
                  320                     325                 330  
  
 Phe His His Leu Pro Gln Met Glu Thr Leu Met Leu Asn Asn Asn  
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                  350                     355                 360  
  
 Leu Gln Glu Val Gly Leu His Gly Asn Pro Ile Arg Cys Asp Cys  
                  365                     370                 375  
  
 Val Ile Arg Trp Ala Asn Ala Thr Gly Thr Arg Val Arg Phe Ile  
                  380                     385                 390  
  
 Glu Pro Gln Ser Thr Leu Cys Ala Glu Pro Pro Asp Leu Gln Arg  
                  395                     400                 405  
  
 Leu Pro Val Arg Glu Val Pro Phe Arg Glu Met Thr Asp His Cys

410	415	420
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425	430	435
Ala Ser Gly Glu Ser Met Val Leu His Cys Arg Ala Leu Ala Glu		
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Pro Glu Pro Glu Ile Tyr Trp Val Thr Pro Ala Gly Leu Arg Leu		
455	460	465
Thr Pro Ala His Ala Gly Arg Arg Tyr Arg Val Tyr Pro Glu Gly		
470	475	480
Thr Leu Glu Leu Arg Arg Val Thr Ala Glu Glu Ala Gly Leu Tyr		
485	490	495
Thr Cys Val Ala Gln Asn Leu Val Gly Ala Asp Thr Lys Thr Val		
500	505	510
Ser Val Val Val Gly Arg Ala Leu Leu Gln Pro Gly Arg Asp Glu		
515	520	525
Gly Gln Gly Leu Glu Leu Arg Val Gln Glu Thr His Pro Tyr His		
530	535	540
Ile Leu Leu Ser Trp Val Thr Pro Pro Asn Thr Val Ser Thr Asn		
545	550	555
Leu Thr Trp Ser Ser Ala Ser Ser Leu Arg Gly Gln Gly Ala Thr		
560	565	570
Ala Leu Ala Arg Leu Pro Arg Gly Thr His Ser Tyr Asn Ile Thr		
575	580	585
Arg Leu Leu Gln Ala Thr Glu Tyr Trp Ala Cys Leu Gln Val Ala		
590	595	600
Phe Ala Asp Ala His Thr Gln Leu Ala Cys Val Trp Ala Arg Thr		
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Lys Glu Ala Thr Ser Cys His Arg Ala Leu Gly Asp Arg Pro Gly		
620	625	630
Leu Ile Ala Ile Leu Ala Leu Ala Val Leu Leu Leu Ala Ala Gly		
635	640	645
Leu Ala Ala His Leu Gly Thr Gly Gln Pro Arg Lys Gly Val Gly		
650	655	660
Gly Arg Arg Pro Leu Pro Pro Ala Trp Ala Phe Trp Gly Trp Ser		
665	670	675

Ala Pro Ser Val Arg Val Val Ser Ala Pro Leu Val Leu Pro Trp  
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<211> 24

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<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 247

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<210> 249

<211> 3401

<212> DNA

<213> Homo Sapien

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 <211> 546  
 <212> PRT  
 <213> Homo Sapien  
 <400> 250  
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 Cys Tyr Thr Val Tyr Tyr Val His Asn Ile Lys Phe Asp Val Asp  
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 Cys Thr Val Asp Ile Glu Ser Leu Thr Gly Tyr Arg Thr Tyr Arg  
 35 40 45  
 Cys Ala His Pro Leu Ala Thr Leu Phe Lys Ile Leu Ala Ser Phe  
 50 55 60  
 Tyr Ile Ser Leu Val Ile Phe Tyr Gly Leu Ile Cys Met Tyr Thr  
 65 70 75  
 Leu Trp Trp Met Leu Arg Arg Ser Leu Lys Lys Tyr Ser Phe Glu  
 80 85 90  
 Ser Ile Arg Glu Glu Ser Ser Tyr Ser Asp Ile Pro Asp Val Lys

95	100	105
Asn Asp Phe Ala Phe Met Leu His Leu Ile Asp Gln Tyr Asp Pro		
110	115	120
Leu Tyr Ser Lys Arg Phe Ala Val Phe Leu Ser Glu Val Ser Glu		
125	130	135
Asn Lys Leu Arg Gln Leu Asn Leu Asn Asn Glu Trp Thr Leu Asp		
140	145	150
Lys Leu Arg Gln Arg Leu Thr Lys Asn Ala Gln Asp Lys Leu Glu		
155	160	165
Leu His Leu Phe Met Leu Ser Gly Ile Pro Asp Thr Val Phe Asp		
170	175	180
Leu Val Glu Leu Glu Val Leu Lys Leu Glu Leu Ile Pro Asp Val		
185	190	195
Thr Ile Pro Pro Ser Ile Ala Gln Leu Thr Gly Leu Lys Glu Leu		
200	205	210
Trp Leu Tyr His Thr Ala Ala Lys Ile Glu Ala Pro Ala Leu Ala		
215	220	225
Phe Leu Arg Glu Asn Leu Arg Ala Leu His Ile Lys Phe Thr Asp		
230	235	240
Ile Lys Glu Ile Pro Leu Trp Ile Tyr Ser Leu Lys Thr Leu Glu		
245	250	255
Glu Leu His Leu Thr Gly Asn Leu Ser Ala Glu Asn Asn Arg Tyr		
260	265	270
Ile Val Ile Asp Gly Leu Arg Glu Leu Lys Arg Leu Lys Val Leu		
275	280	285
Arg Leu Lys Ser Asn Leu Ser Lys Leu Pro Gln Val Val Thr Asp		
290	295	300
Val Gly Val His Leu Gln Lys Leu Ser Ile Asn Asn Glu Gly Thr		
305	310	315
Lys Leu Ile Val Leu Asn Ser Leu Lys Lys Met Ala Asn Leu Thr		
320	325	330
Glu Leu Glu Leu Ile Arg Cys Asp Leu Glu Arg Ile Pro His Ser		
335	340	345
Ile Phe Ser Leu His Asn Leu Gln Glu Ile Asp Leu Lys Asp Asn		
350	355	360

Asn Leu Lys Thr Ile Glu Glu Ile Ile Ser Phe Gln His Leu His  
                   365                     370                 375  
  
 Arg Leu Thr Cys Leu Lys Leu Trp Tyr Asn His Ile Ala Tyr Ile  
                   380                     385                 390  
  
 Pro Ile Gln Ile Gly Asn Leu Thr Asn Leu Glu Arg Leu Tyr Leu  
                   395                     400                 405  
  
 Asn Arg Asn Lys Ile Glu Lys Ile Pro Thr Gln Leu Phe Tyr Cys  
                   410                     415                 420  
  
 Arg Lys Leu Arg Tyr Leu Asp Leu Ser His Asn Asn Leu Thr Phe  
                   425                     430                 435  
  
 Leu Pro Ala Asp Ile Gly Leu Leu Gln Asn Leu Gln Asn Leu Ala  
                   440                     445                 450  
  
 Ile Thr Ala Asn Arg Ile Glu Thr Leu Pro Pro Glu Leu Phe Gln  
                   455                     460                 465  
  
 Cys Arg Lys Leu Arg Ala Leu His Leu Gly Asn Asn Val Leu Gln  
                   470                     475                 480  
  
 Ser Leu Pro Ser Arg Val Gly Glu Leu Thr Asn Leu Thr Gln Ile  
                   485                     490                 495  
  
 Glu Leu Arg Gly Asn Arg Leu Glu Cys Leu Pro Val Glu Leu Gly  
                   500                     505                 510  
  
 Glu Cys Pro Leu Leu Lys Arg Ser Gly Leu Val Val Glu Glu Asp  
                   515                     520                 525  
  
 Leu Phe Asn Thr Leu Pro Pro Glu Val Lys Glu Arg Leu Trp Arg  
                   530                     535                 540  
  
 Ala Asp Lys Glu Gln Ala  
                   545  
  
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 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic Oligonucleotide Probe  
  
 <400> 251  
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 <210> 252  
 <211> 24

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 252  
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<210> 253  
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<212> DNA  
<213> Artificial Sequence

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<400> 253  
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<210> 254  
<211> 1650  
<212> DNA  
<213> Homo Sapien

<400> 254  
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tgggattatg tgacggtccg caaggatgcc tacatgttct ggtggctcta 200  
ttatgccacc aactcctgca agaacttctc agaactgccc ctggtcatgt 250  
ggcttcaggc cggtccaggc ggttctagca ctggatttgg aaacttttag 300  
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<210> 255  
<211> 452  
<212> PRT  
<213> Homo Sapien

<400> 255  
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20							25						30

Trp	Pro	Thr	Glu	Glu	Gly	Lys	Glu	Val	Trp	Asp	Tyr	Val	Thr	Val
35								40						45

Arg Lys Asp Ala Tyr Met Phe Trp Trp Leu Tyr Tyr Ala Thr Asn  
                   50                      55                      60

Ser Cys Lys Asn Phe Ser Glu Leu Pro Leu Val Met Trp Leu Gln  
                   65                      70                      75

Gly Gly Pro Gly Gly Ser Ser Thr Gly Phe Gly Asn Phe Glu Glu  
                   80                      85                      90

Ile Gly Pro Leu Asp Ser Asp Leu Lys Pro Arg Lys Thr Thr Trp  
                   95                      100                    105

Leu Gln Ala Ala Ser Leu Leu Phe Val Asp Asn Pro Val Gly Thr  
                   110                      115                    120

Gly Phe Ser Tyr Val Asn Gly Ser Gly Ala Tyr Ala Lys Asp Leu  
                   125                      130                    135

Ala Met Val Ala Ser Asp Met Met Val Leu Leu Lys Thr Phe Phe  
                   140                      145                    150

Ser Cys His Lys Glu Phe Gln Thr Val Pro Phe Tyr Ile Phe Ser  
                   155                      160                    165

Glu Ser Tyr Gly Gly Lys Met Ala Ala Gly Ile Gly Leu Glu Leu  
                   170                      175                    180

Tyr Lys Ala Ile Gln Arg Gly Thr Ile Lys Cys Asn Phe Ala Gly  
                   185                      190                    195

Val Ala Leu Gly Asp Ser Trp Ile Ser Pro Val Asp Ser Val Leu  
                   200                      205                    210

Ser Trp Gly Pro Tyr Leu Tyr Ser Met Ser Leu Leu Glu Asp Lys  
                   215                      220                    225

Gly Leu Ala Glu Val Ser Lys Val Ala Glu Gln Val Leu Asn Ala  
                   230                      235                    240

Val Asn Lys Gly Leu Tyr Arg Glu Ala Thr Glu Leu Trp Gly Lys  
                   245                      250                    255

Ala Glu Met Ile Ile Glu Gln Asn Thr Asp Gly Val Asn Phe Tyr  
                   260                      265                    270

Asn Ile Leu Thr Lys Ser Thr Pro Thr Ser Thr Met Glu Ser Ser  
                   275                      280                    285

Leu Glu Phe Thr Gln Ser His Leu Val Cys Leu Cys Gln Arg His  
                   290                      295                    300

Val Arg His Leu Gln Arg Asp Ala Leu Ser Gln Leu Met Asn Gly

305	310	315
Pro Ile Arg Lys Lys Leu Lys Ile Ile Pro Glu Asp Gln Ser Trp		
320	325	330
Gly Gly Gln Ala Thr Asn Val Phe Val Asn Met Glu Glu Asp Phe		
335	340	345
Met Lys Pro Val Ile Ser Ile Val Asp Glu Leu Leu Glu Ala Gly		
350	355	360
Ile Asn Val Thr Val Tyr Asn Gly Gln Leu Asp Leu Ile Val Asp		
365	370	375
Thr Met Gly Gln Glu Ala Trp Val Arg Lys Leu Lys Trp Pro Glu		
380	385	390
Leu Pro Lys Phe Ser Gln Leu Lys Trp Lys Ala Leu Tyr Ser Asp		
395	400	405
Pro Lys Ser Leu Glu Thr Ser Ala Phe Val Lys Ser Tyr Lys Asn		
410	415	420
Leu Ala Phe Tyr Trp Ile Leu Lys Ala Gly His Met Val Pro Ser		
425	430	435
Asp Gln Gly Asp Met Ala Leu Lys Met Met Arg Leu Val Thr Gln		
440	445	450
 Gln Glu		

<210> 256

<211> 1100

<212> DNA

<213> Homo Sapien

<400> 256

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tggagaggac gccgaactcg ggcgttggcc gtggcagggg agcctgcgcc 200

tgtgggattc ccacgtatgc ggagtgagcc tgctcagcca ccgctggca 250

ctcacggcgg cgcaactgctt tgaaacctat agtacacctta gtgatccctc 300

cgggtggatg gtccagtttq gccagctgac ttccatgccca tccttctgga 350

gcctgcaggc ctactacacc cgttacttcg tatcgaatat ctatctgagc 400

cctcgctacc tgggaaattc accctatgac attgccttgg tgaagctgtc 450  
tgcacctgtc acctacacta aacacatcca gcccacatgt ctccaggcct 500  
ccacatttga gtttgagaac cgAACAGACT gctgggtgac tggctggggg 550  
tacatcaaag aggatgaggg actgccatct ccccacaccc tccaggaagt 600  
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<210> 257  
<211> 314  
<212> PRT  
<213> Homo Sapien

<400> 257

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Ala	Gly	Leu	Arg	Lys	Pro	Glu	Ser	Gln	Glu	Ala	Ala	Pro	Leu	Ser
					20				25					30

Gly	Pro	Cys	Gly	Arg	Arg	Val	Ile	Thr	Ser	Arg	Ile	Val	Gly	Gly
						35			40					45

Glu	Asp	Ala	Glu	Leu	Gly	Arg	Trp	Pro	Trp	Gln	Gly	Ser	Leu	Arg
						50			55					60

Leu	Trp	Asp	Ser	His	Val	Cys	Gly	Val	Ser	Leu	Leu	Ser	His	Arg
						65			70					75

Trp	Ala	Leu	Thr	Ala	Ala	His	Cys	Phe	Glu	Thr	Tyr	Ser	Asp	Leu
							80			85				90

Ser Asp Pro Ser Gly Trp Met Val Gln Phe Gly Gln Leu Thr Ser  
 95 100 105  
 Met Pro Ser Phe Trp Ser Leu Gln Ala Tyr Tyr Thr Arg Tyr Phe  
 110 115 120  
 Val Ser Asn Ile Tyr Leu Ser Pro Arg Tyr Leu Gly Asn Ser Pro  
 125 130 135  
 Tyr Asp Ile Ala Leu Val Lys Leu Ser Ala Pro Val Thr Tyr Thr  
 140 145 150  
 Lys His Ile Gln Pro Ile Cys Leu Gln Ala Ser Thr Phe Glu Phe  
 155 160 165  
 Glu Asn Arg Thr Asp Cys Trp Val Thr Gly Trp Gly Tyr Ile Lys  
 170 175 180  
 Glu Asp Glu Ala Leu Pro Ser Pro His Thr Leu Gln Glu Val Gln  
 185 190 195  
 Val Ala Ile Ile Asn Asn Ser Met Cys Asn His Leu Phe Leu Lys  
 200 205 210  
 Tyr Ser Phe Arg Lys Asp Ile Phe Gly Asp Met Val Cys Ala Gly  
 215 220 225  
 Asn Ala Gln Gly Gly Lys Asp Ala Cys Phe Gly Asp Ser Gly Gly  
 230 235 240  
 Pro Leu Ala Cys Asn Lys Asn Gly Leu Trp Tyr Gln Ile Gly Val  
 245 250 255  
 Val Ser Trp Gly Val Gly Cys Gly Arg Pro Asn Arg Pro Gly Val  
 260 265 270  
 Tyr Thr Asn Ile Ser His His Phe Glu Trp Ile Gln Lys Leu Met  
 275 280 285  
 Ala Gln Ser Gly Met Ser Gln Pro Asp Pro Ser Trp Pro Leu Leu  
 290 295 300  
 Phe Phe Pro Leu Leu Trp Ala Leu Pro Leu Leu Gly Pro Val  
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&lt;210&gt; 258

&lt;211&gt; 2427

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;400&gt; 258

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 aatgattgat acctcaaatg taaaaaa 2427

&lt;210&gt; 259

&lt;211&gt; 556

&lt;212&gt; PRT

&lt;213&gt; Homo Sapien

&lt;400&gt; 259

Met	Gly	Leu	Gln
Ala	Cys	Leu	Leu
Leu	Gly	Leu	Phe
		Ala	Leu
		Ile	Leu

1	5	10	15
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Ser	Gly	Lys	Cys
Ser	Tyr	Ser	Pro
		Glu	Pro
		Asp	Gln
			Arg
			Thr

20	25	30
Leu Pro Pro Gly Trp Val Ser Leu Gly Arg Ala Asp Pro Glu Glu		
35	40	45
Glu Leu Ser Leu Thr Phe Ala Leu Arg Gln Gln Asn Val Glu Arg		
50	55	60
Leu Ser Glu Leu Val Gln Ala Val Ser Asp Pro Ser Ser Pro Gln		
65	70	75
Tyr Gly Lys Tyr Leu Thr Leu Glu Asn Val Ala Asp Leu Val Arg		
80	85	90
Pro Ser Pro Leu Thr Leu His Thr Val Gln Lys Trp Leu Leu Ala		
95	100	105
Ala Gly Ala Gln Lys Cys His Ser Val Ile Thr Gln Asp Phe Leu		
110	115	120
Thr Cys Trp Leu Ser Ile Arg Gln Ala Glu Leu Leu Leu Pro Gly		
125	130	135
Ala Glu Phe His His Tyr Val Gly Gly Pro Thr Glu Thr His Val		
140	145	150
Val Arg Ser Pro His Pro Tyr Gln Leu Pro Gln Ala Leu Ala Pro		
155	160	165
His Val Asp Phe Val Gly Gly Leu His Arg Phe Pro Pro Thr Ser		
170	175	180
Ser Leu Arg Gln Arg Pro Glu Pro Gln Val Thr Gly Thr Val Gly		
185	190	195
Leu His Leu Gly Val Thr Pro Ser Val Ile Arg Lys Arg Tyr Asn		
200	205	210
Leu Thr Ser Gln Asp Val Gly Ser Gly Thr Ser Asn Asn Ser Gln		
215	220	225
Ala Cys Ala Gln Phe Leu Glu Gln Tyr Phe His Asp Ser Asp Leu		
230	235	240
Ala Gln Phe Met Arg Leu Phe Gly Gly Asn Phe Ala His Gln Ala		
245	250	255
Ser Val Ala Arg Val Val Gly Gln Gln Gly Arg Gly Arg Ala Gly		
260	265	270
Ile Glu Ala Ser Leu Asp Val Gln Tyr Leu Met Ser Ala Gly Ala		
275	280	285

195 190 185 180 175 170 165 160 155 150 145 140 135 130 125 120 115 110 105 100 95 90 85 80 75 70 65 60 55 50 45 40 35 30 25 20 15 10 5 1

Asn Ile Ser Thr Trp Val Tyr Ser Ser Pro Gly Arg His Glu Gly  
 290 295 300  
 Gln Glu Pro Phe Leu Gln Trp Leu Met Leu Leu Ser Asn Glu Ser  
 305 310 315  
 Ala Leu Pro His Val His Thr Val Ser Tyr Gly Asp Asp Glu Asp  
 320 325 330  
 Ser Leu Ser Ser Ala Tyr Ile Gln Arg Val Asn Thr Glu Leu Met  
 335 340 345  
 Lys Ala Ala Ala Arg Gly Leu Thr Leu Leu Phe Ala Ser Gly Asp  
 350 355 360  
 Ser Gly Ala Gly Cys Trp Ser Val Ser Gly Arg His Gln Phe Arg  
 365 370 375  
 Pro Thr Phe Pro Ala Ser Ser Pro Tyr Val Thr Thr Val Gly Gly  
 380 385 390  
 Thr Ser Phe Gln Glu Pro Phe Leu Ile Thr Asn Glu Ile Val Asp  
 395 400 405  
 Tyr Ile Ser Gly Gly Phe Ser Asn Val Phe Pro Arg Pro Ser  
 410 415 420  
 Tyr Gln Glu Glu Ala Val Thr Lys Phe Leu Ser Ser Ser Pro His  
 425 430 435  
 Leu Pro Pro Ser Ser Tyr Phe Asn Ala Ser Gly Arg Ala Tyr Pro  
 440 445 450  
 Asp Val Ala Ala Leu Ser Asp Gly Tyr Trp Val Val Ser Asn Arg  
 455 460 465  
 Val Pro Ile Pro Trp Val Ser Gly Thr Ser Ala Ser Thr Pro Val  
 470 475 480  
 Phe Gly Gly Ile Leu Ser Leu Ile Asn Glu His Arg Ile Leu Ser  
 485 490 495  
 Gly Arg Pro Pro Leu Gly Phe Leu Asn Pro Arg Leu Tyr Gln Gln  
 500 505 510  
 His Gly Ala Gly Leu Phe Asp Val Thr Arg Gly Cys His Glu Ser  
 515 520 525  
 Cys Leu Asp Glu Glu Val Glu Gly Gln Gly Phe Cys Ser Gly Pro  
 530 535 540  
 Gly Trp Asp Pro Val Thr Gly Trp Gly Thr Pro Thr Ser Gln Leu  
 545 550 555

## Cys

<210> 260  
<211> 1638  
<212> DNA  
<213> Homo Sapien

<400> 260  
gccgcgcgt ctctccggc gcccacacct gtctgagcgg cgcagcgagc 50  
cgccggcccg gggggctgct cggcgcgaa cagtgcgtt catggcagg 100  
attccagggc tcctcttcct tctttttt ctgctctgtt ctgttggca 150  
agtgagccct tacagtgccc cctggaaacc cacttggct gcataaccgc 200  
tccctgtcgt cttgccccag tctaccctca atttagccaa gccagacttt 250  
ggagccgaag ccaaattaga agtatcttct tcatgtggac cccagtgtca 300  
taaggaaact ccactgccc cttacgaaga ggccaagcaa tatctgttctt 350  
atgaaacgct ctatgccaat ggcagccgca cagagacgca ggtgggcatc 400  
tacatcctca gcagtagtgg agatggggcc caacaccgag actcagggtc 450  
ttcaggaaag tctcgaagga agcggcagat ttatggctat gacagcagg 500  
tcagcatttt tggaaaggac ttccctgctca actaccctt ctcaacatca 550  
gtgaagttat ccacgggctg caccggcacc ctgggtggcag agaagcatgt 600  
cctcacagct gcccactgca tacacgatgg aaaaacctat gtgaaaggaa 650  
cccagaagct tcgagtgccc ttccctaaagc ccaagttaa agatgggttgt 700  
cgaggggcca acgactccac ttccagccatg cccgagcaga tgaaattca 750  
gtggatccgg gtgaaacgca cccatgtgcc caagggttgg atcaagggca 800  
atgccaatga catcgccatg gattatgatt atgccccttc ggaactcaaa 850  
aagccccaca agagaaaatt tatgaagatt ggggtgagcc ttccctgctaa 900  
gcagctgcca gggggcagaa ttccattctc tggttatgac aatgaccgac 950  
caggcaattt ggtgtatcgc ttctgtgacg tcaaagacga gacctatgac 1000  
ttgctctacc agcaatgcga tgcccgccca ggggcccagcg ggtctggggt 1050  
ctatgtgagg atgtggaaga gacagcagca gaagtgggag cgaaaaattha 1100

ttggcattt ttcagggcac cagtgggtgg acatgaatgg ttccccacag 1150  
 gatttcaacg tggctgtcag aatcactcct ctcaaatacg cccagatttg 1200  
 ctattggatt aaaggaaaact acctggattt tagggagggg tgacacagtg 1250  
 ttccctcctg gcagcaatta agggtcttca tgttcttatt ttaggagagg 1300  
 ccaaattgtt ttttgcatt ggcgtgcaca cgtgtgtgtg tgtgtgtgtg 1350  
 tgtgtgttaag gtgtcttata atcttttacc tatttcttac aattgcaaga 1400  
 tgactggctt tactatttga aaactggttt gtgtatcata tcatastatca 1450  
 tttaaggcgt ttgaaggcat acttttgcatt agaaataaaaa aaaatactga 1500  
 tttggggcaa tgaggaatat ttgacaatta agttaatctt cacgttttg 1550  
 caaactttga tttttatttc atctgaacctt gtttcaaaga tttatattaa 1600  
 atatttggca tacaagagat atgaaaaaaaaaaaaaaa 1638

&lt;210&gt; 261

&lt;211&gt; 383

&lt;212&gt; PRT

&lt;213&gt; Homo Sapien

&lt;400&gt; 261

Met	Ala	Gly	Ile	Pro	Gly	Leu	Leu	Phe	Leu	Leu	Phe	Leu	Leu
1													15

Cys	Ala	Val	Gly	Gln	Val	Ser	Pro	Tyr	Ser	Ala	Pro	Trp	Lys	Pro
														30
20														

Thr	Trp	Pro	Ala	Tyr	Arg	Leu	Pro	Val	Val	Leu	Pro	Gln	Ser	Thr
														45
35														

Leu	Asn	Leu	Ala	Lys	Pro	Asp	Phe	Gly	Ala	Glu	Ala	Lys	Leu	Glu
														60
50														

Val	Ser	Ser	Ser	Cys	Gly	Pro	Gln	Cys	His	Lys	Gly	Thr	Pro	Leu
														75
65														

Pro	Thr	Tyr	Glu	Glu	Ala	Lys	Gln	Tyr	Leu	Ser	Tyr	Glu	Thr	Leu
														90
80														

Tyr	Ala	Asn	Gly	Ser	Arg	Thr	Glu	Thr	Gln	Val	Gly	Ile	Tyr	Ile
														105
95														

Leu	Ser	Ser	Ser	Gly	Asp	Gly	Ala	Gln	His	Arg	Asp	Ser	Gly	Ser
														120
110														

Ser Gly Lys Ser Arg Arg Lys Arg Gln Ile Tyr Gly Tyr Asp Ser  
                  125                     130                     135  
 Arg Phe Ser Ile Phe Gly Lys Asp Phe Leu Leu Asn Tyr Pro Phe  
                  140                     145                     150  
 Ser Thr Ser Val Lys Leu Ser Thr Gly Cys Thr Gly Thr Leu Val  
                  155                     160                     165  
 Ala Glu Lys His Val Leu Thr Ala Ala His Cys Ile His Asp Gly  
                  170                     175                     180  
 Lys Thr Tyr Val Lys Gly Thr Gln Lys Leu Arg Val Gly Phe Leu  
                  185                     190                     195  
 Lys Pro Lys Phe Lys Asp Gly Gly Arg Gly Ala Asn Asp Ser Thr  
                  200                     205                     210  
 Ser Ala Met Pro Glu Gln Met Lys Phe Gln Trp Ile Arg Val Lys  
                  215                     220                     225  
 Arg Thr His Val Pro Lys Gly Trp Ile Lys Gly Asn Ala Asn Asp  
                  230                     235                     240  
 Ile Gly Met Asp Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Lys Pro  
                  245                     250                     255  
 His Lys Arg Lys Phe Met Lys Ile Gly Val Ser Pro Pro Ala Lys  
                  260                     265                     270  
 Gln Leu Pro Gly Gly Arg Ile His Phe Ser Gly Tyr Asp Asn Asp  
                  275                     280                     285  
 Arg Pro Gly Asn Leu Val Tyr Arg Phe Cys Asp Val Lys Asp Glu  
                  290                     295                     300  
 Thr Tyr Asp Leu Leu Tyr Gln Gln Cys Asp Ala Gln Pro Gly Ala  
                  305                     310                     315  
 Ser Gly Ser Gly Val Tyr Val Arg Met Trp Lys Arg Gln Gln Gln  
                  320                     325                     330  
 Lys Trp Glu Arg Lys Ile Ile Gly Ile Phe Ser Gly His Gln Trp  
                  335                     340                     345  
 Val Asp Met Asn Gly Ser Pro Gln Asp Phe Asn Val Ala Val Arg  
                  350                     355                     360  
 Ile Thr Pro Leu Lys Tyr Ala Gln Ile Cys Tyr Trp Ile Lys Gly  
                  365                     370                     375  
 Asn Tyr Leu Asp Cys Arg Glu Gly  
                  380

<210> 262  
<211> 1378  
<212> DNA  
<213> Homo Sapien

<400> 262  
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ccatggtggt ttctggagcg ccccccagccc tgggtggggg ctgtctcgcc 100  
accttcacct ccctgctgct gctggcgctcg acagccatcc tcaatgcggc 150  
caggataacct gttccccag cctgtggaa gccccagcag ctgaaccggg 200  
ttgtggcgcc cgaggacacgc actgacacgcg agtggccctg gatcgtgagc 250  
atccagaaga atgggaccca ccactgcgcga ggttctctgc tcaccagccg 300  
ctgggtgatc actgctgccc actgtttcaa ggacaacctg aacaaaccat 350  
acctgttctc tgtgctgctg ggggcctggc agctgggaa ccctggctct 400  
cggtcccaga aggtgggtgt tgccctgggtg gagccccacc ctgtgtattc 450  
ctggaaggaa ggtgcctgtg cagacattgc cctggtgctg ctcgagcgt 500  
ccatacagtt ctcagagcgg gtcctgcccc tctgcctacc tgatgcctct 550  
atccacactcc ctccaaacac ccactgctgg atctcaggct gggggagcat 600  
ccaagatgga gttcccttgc cccaccctca gaccctgcag aagctgaagg 650  
ttcctatcat cgactcgaa gtctgcagcc atctgtactg gcggggagca 700  
ggacagggac ccatcactga ggacatgctg tgtgcggct acttggaggg 750  
ggagcgggat gcttgtctgg gcgactccgg gggccccctc atgtgccagg 800  
tggacggcgc ctggctgctg gccggcatca tcagctgggg cgagggctgt 850  
gccgagcgcga acaggccccgg ggtctacatc agcctctctg cgcaccgctc 900  
ctgggtggag aagatcgtgc aaggggtgca gctccgcggg cgcgctcagg 950  
gggggtggggc cctcaggca ccgagccagg gctctggggc cgccgcgcgc 1000  
tccttagggcg cagcgggacg cggggctcgg atctgaaagg cggccagatc 1050  
cacatctgga tctggatctg cggcgccctc gggcggttcc ccccgccgta 1100  
aataggctca tctacacctta cctctggggg cccggacggc tgctgcggaa 1150

agaaaaacccc ctccccgacc cgcccgacgg cctcaggccc ccctccaagg 1200  
 catcaggccc cgcccaacgg cctcatgtcc cgcggccac gacttccggc 1250  
 cccgcccccg ggccccagcg cttttgtgta tataaatgtt aatgattttt 1300  
 ataggtattt gtaaccctgc ccacatatct tatttattcc tccaatttca 1350  
 ataaaattttt tattctccaa aaaaaaaaa 1378

<210> 263  
 <211> 317  
 <212> PRT  
 <213> Homo Sapien

<400> 263

Met	Val	Val	Ser	Gly	Ala	Pro	Pro	Ala	Leu	Gly	Gly	Gly	Cys	Leu	
1					5				10					15	
Gly	Thr	Phe	Thr	Ser	Leu	Leu	Leu	Leu	Ala	Ser	Thr	Ala	Ile	Leu	
					20				25					30	
Asn	Ala	Ala	Arg	Ile	Pro	Val	Pro	Pro	Ala	Cys	Gly	Lys	Pro	Gln	
					35				40					45	
Gln	Leu	Asn	Arg	Val	Val	Gly	Gly	Glu	Asp	Ser	Thr	Asp	Ser	Glu	
					50				55					60	
Trp	Pro	Trp	Ile	Val	Ser	Ile	Gln	Lys	Asn	Gly	Thr	His	His	Cys	
					65				70					75	
Ala	Gly	Ser	Leu	Leu	Thr	Ser	Arg	Trp	Val	Ile	Thr	Ala	Ala	His	
					80				85					90	
Cys	Phe	Lys	Asp	Asn	Leu	Asn	Lys	Pro	Tyr	Leu	Phe	Ser	Val	Leu	
					95				100					105	
Leu	Gly	Ala	Trp	Gln	Leu	Gly	Asn	Pro	Gly	Ser	Arg	Ser	Gln	Lys	
					110				115					120	
Val	Gly	Val	Ala	Trp	Val	Glu	Pro	His	Pro	Val	Tyr	Ser	Trp	Lys	
					125				130					135	
Glu	Gly	Ala	Cys	Ala	Asp	Ile	Ala	Leu	Val	Arg	Leu	Glu	Arg	Ser	
					140				145					150	
Ile	Gln	Phe	Ser	Glu	Arg	Val	Leu	Pro	Ile	Cys	Leu	Pro	Asp	Ala	
					155				160					165	
Ser	Ile	His	Leu	Pro	Pro	Asn	Thr	His	Cys	Trp	Ile	Ser	Gly	Trp	
					170				175					180	

Gly Ser Ile Gln Asp Gly Val Pro Leu Pro His Pro Gln Thr Leu  
185 190 195  
Gln Lys Leu Lys Val Pro Ile Ile Asp Ser Glu Val Cys Ser His  
200 205 210  
Leu Tyr Trp Arg Gly Ala Gly Gln Gly Pro Ile Thr Glu Asp Met  
215 220 225  
Leu Cys Ala Gly Tyr Leu Glu Gly Glu Arg Asp Ala Cys Leu Gly  
230 235 240  
Asp Ser Gly Gly Pro Leu Met Cys Gln Val Asp Gly Ala Trp Leu  
245 250 255  
Leu Ala Gly Ile Ile Ser Trp Gly Glu Gly Cys Ala Glu Arg Asn  
260 265 270  
Arg Pro Gly Val Tyr Ile Ser Leu Ser Ala His Arg Ser Trp Val  
275 280 285  
Glu Lys Ile Val Gln Gly Val Gln Leu Arg Gly Arg Ala Gln Gly  
290 295 300  
Gly Gly Ala Leu Arg Ala Pro Ser Gln Gly Ser Gly Ala Ala Ala  
305 310 315

Arg Ser

<210> 264

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 264

gtccgcaagg atgcctacat gttc 24

<210> 265

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 265

gcagaggtgt ctaaggttg 19

<210> 266

<211> 24

<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic Oligonucleotide Probe  
  
<400> 266  
agctctagac caatgccagc ttcc 24  
  
<210> 267  
<211> 45  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic Oligonucleotide Probe  
  
<400> 267  
gccaccaact cctgcaagaa cttctcagaa ctgcccctgg tcatg 45  
  
<210> 268  
<211> 25  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic Oligonucleotide Probe  
  
<400> 268  
gggaaattca ccctatgaca ttgcc 25  
  
<210> 269  
<211> 24  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic Oligonucleotide Probe  
  
<400> 269  
aatgccctg caagcatcaa ctgg 24  
  
<210> 270  
<211> 50  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic Oligonucleotide Probe  
  
<400> 270  
gcacctgtca cctacactaa acacatccag cccatctgtc tccaggcctc 50

<210> 271  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 271  
gcggaagggc agaatggac tccaaag 26

<210> 272  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 272  
cagccctgcc acatgtgc 18

<210> 273  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 273  
tactgggtgg tcagcaac 18

<210> 274  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 274  
ggcgaagagc agggtgagac cccg 24

<210> 275  
<211> 45

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 275  
gcctctatcc tctctggcaa atgcagttac agcccgagc ccgac 45

<210> 276  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 276  
ggcaggat tccagggttc c 21

<210> 277  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 277  
ggctatgaca gcaggttc 18

<210> 278  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 278  
tgacaatgac cgaccagg 18

<210> 279  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 279  
gcatcgcatt gctggtagag caag 24

<210> 280  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 280  
ttacagtgcc ccctggaaac ccacttggcc tgcataaccgc ctccc 45

<210> 281

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 281  
cgtctcgagc gtcataaca gttccattgc ccca 34

<210> 282

<211> 61

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 282

tggaggggga gcgggatgct tgtctggcg actccggggg cccccatcg 50

tgccagggtgg a 61

<210> 283

<211> 119

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 283

ccctcagacc ctgcagaagc tgaaggttcc tatcatcgac tcggaagtct 50

gcagccatct gtactggcg ggagcaggac agggacccat cactgaggac 100

atgctgtgtg ccggctact 119

<210> 284

<211> 1875

<212> DNA

<213> Homo Sapien

<400> 284

gacggctggc caccatgcac ggctcctgca gttccctgat gttctgctg 50

ccgctactgc tactgctggc ggccaccaca ggccccgttg gagccctcac 100

agatgaggag aaacgttga tggtgagct gcacaaccc taccgggccc 150  
aggatatcccc gacggcctca gacatgctgc acatgagatg ggacgaggag 200  
ctggccgcct tcgccaaggc ctacgcacgg cagtgcgtgt gggccacaa 250  
caaggagcgc gggcgccgag gcgagaatct gttcgccatc acagacgagg 300  
gcatggacgt gccgctggcc atggaggagt ggcaccacga gcgtgagcac 350  
tacaacctca gcgcgcac 400  
cacgcaggtg gtagggcca agacagagag gatcggctgt gttcccact 450  
tctgtgagaa gctccagggt gttgaggaga ccaacatcga attactggtg 500  
tgcaactatg agcctccggg gaacgtgaag gggaaacggc cttaccagga 550  
ggggactccg tgctccaat gtccctctgg ctaccactgc aagaactccc 600  
tctgtgaacc catcgaaagc ccgaaagatg ctcaggattt gccttacctg 650  
gtaactgagg ccccatcctt ccggcgact gaagcatcag actctaggaa 700  
aatgggtact ctttcttccc tagcaacggg gattccggct ttcttggtaa 750  
cagaggctc aggctccctg gcaaccaagg ctctgcctgc tgtggaaacc 800  
caggccccaa ctcccttagc aacgaaagac ccgcctcca tggcaacaga 850  
ggctccaccc tgcgtaacaa ctgaggtccc ttccatccgc 900  
gcctgcctc cttggatgag gagccagttt cttcccttccaa atcgacccat 950  
gttccatcc caaaatcagc agacaaagtg acagacaaaa caaaagtgcc 1000  
ctcttaggagc ccagagaact ctctggaccc caagatgtcc ctgacagggg 1050  
caaggaaact cttcccttccaa gcccaggagg aggctgaggg tgaggctgag 1100  
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gccagggtgag ctgcaggcca cactggacca cacggggcac acctcctcca 1200  
agtccctgccc caatttcccc aatacctctg ccacccgctaa tgccacgggt 1250  
gggcgtgccc tggctctgca gtcgtccttgc ccaggtgcag agggccctga 1300  
caaggcttagc gttgtgtcag ggctgaactc gggccctgggt catgtgtggg 1350  
gccttccttccctt gggactactg ctctgcctc ctctgggtt ggctggaaatc 1400

ttctgaatgg gataccactc aaagggtgaa gaggtcagct gtcctcctgt 1450  
 catttcccc accctgtccc cagcccctaa acaagatact tcttggtaa 1500  
 ggccctccgg aaggaaagg ctacggggca tgtgcctcat cacaccatcc 1550  
 atcctggagg cacaaggcct ggctggctgc gagtcagga ggccgcctga 1600  
 ggactgcaca ccgggcccac acctctcctg cccctccctc ctgagtcctg 1650  
 ggggtggag gatttggagg agctcactgc ctacctggcc tggggctgtc 1700  
 tgcccacaca gcatgtgcgc tctccctgag tgcctgtgt a gctggggatg 1750  
 gggattccta gggcagatg aaggacaagc cccactggag tggggttctt 1800  
 tgagtgggg aggcaaggac gagggaaagga aagtaactcc tgactctcca 1850  
 ataaaaaacct gtccaaacctg tgaaa 1875

&lt;210&gt; 285

&lt;211&gt; 463

&lt;212&gt; PRT

&lt;213&gt; Homo Sapien

&lt;400&gt; 285

Met His Gly Ser Cys Ser Phe Leu Met Leu Leu Leu Pro Leu Leu			
1	5	10	15

Leu Leu Leu Val Ala Thr Thr Gly Pro Val Gly Ala Leu Thr Asp			
20	25	30	

Glu Glu Lys Arg Leu Met Val Glu Leu His Asn Leu Tyr Arg Ala			
35	40	45	

Gln Val Ser Pro Thr Ala Ser Asp Met Leu His Met Arg Trp Asp			
50	55	60	

Glu Glu Leu Ala Ala Phe Ala Lys Ala Tyr Ala Arg Gln Cys Val			
65	70	75	

Trp Gly His Asn Lys Glu Arg Gly Arg Arg Gly Glu Asn Leu Phe			
80	85	90	

Ala Ile Thr Asp Glu Gly Met Asp Val Pro Leu Ala Met Glu Glu			
95	100	105	

Trp His His Glu Arg Glu His Tyr Asn Leu Ser Ala Ala Thr Cys			
110	115	120	

Ser Pro Gly Gln Met Cys Gly His Tyr Thr Gln Val Val Trp Ala			
125	130	135	



Ala Thr Ala Asn Ala Thr Gly Gly Arg Ala Leu Ala Leu Gln Ser  
 410 415 420

Ser Leu Pro Gly Ala Glu Gly Pro Asp Lys Pro Ser Val Val Ser  
 425 430 435

Gly Leu Asn Ser Gly Pro Gly His Val Trp Gly Pro Leu Leu Gly  
 440 445 450

Leu Leu Leu Leu Pro Pro Leu Val Leu Ala Gly Ile Phe  
 455 460

<210> 286

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 286

tcctgcagtt tcctgatgc 19

<210> 287

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 287

ctcatattgc acaccagtaa ttcg 24

<210> 288

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 288

atgaggagaa acgtttgatg gtggagctgc acaacctcta ccggg 45

<210> 289

<211> 3662

<212> DNA

<213> Homo Sapien

<400> 289

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tcattctcca agttatggtg gacgtacttc tgggttctc cctctgctg 100  
cttttcaca ttagcagacc ggacttaagt cacaacagat tatctttcat 150  
caaggcaagt tccatgagcc accttcaaag cttcgagaa gtgaaaactga 200  
acaacaatga attggagacc attccaaatc tgggaccagt ctggcaaat 250  
attacacttc ttccttggc tgaaaacagg attgtgaaa tactccctga 300  
acatctgaaa gagttcagt cccttgaaac ttggacacctt agcagcaaca 350  
atattcaga gtcctaaact gcattccag ccctacagct caaatatctg 400  
tatctcaaca gcaaccgagt cacatcaatg gaacctgggt atttgacaa 450  
tttggccaac acactccttg tgttaaagct gaacaggaac cgaatctcag 500  
ctatcccacc caagatgtt aaactgcacc aactgcaaca tctcgaattt 550  
aaccgaaaca agattaaaaa tggatggc ctgacattcc aaggccttgg 600  
tgctctgaag tctctgaaaa tgaaaagaaa tggagtaacg aaacttatgg 650  
atggagctt ttggggctg agcaacatgg aaatttgca gctggaccat 700  
aacaacctaa cagagattac caaaggctgg cttaacggct tgctgatgct 750  
gcaggaactt catctcagcc aaaatgccat caacaggatc agccctgatg 800  
cctggagtt ctgcagaag ctcagtgagc tggacctaac tttcaatcac 850  
ttatcaaggt tagatgattc aagttccctt ggcctaagct tactaaatac 900  
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 tttttaact ttgtttatg caaaaaagta tcttacgtaa attaatgata 3500  
 taaatcatga ttatTTATG tattttata atgccagatt tcttttatg 3550  
 gaaaatgagt tactaaagca ttttaataa tacctgcctt gtaccattt 3600  
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<210> 290  
 <211> 1059  
 <212> PRT  
 <213> Homo Sapien

<400> 290  
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                   20                  25                  30

Ala Ser Ser Met Ser His Leu Gln Ser Leu Arg Glu Val Lys Leu  
                  35                        40                        45

Asn Asn Asn Glu Leu Glu Thr Ile Pro Asn Leu Gly Pro Val Ser  
                  50                        55                        60

Ala Asn Ile Thr Leu Leu Ser Leu Ala Gly Asn Arg Ile Val Glu  
                  65                        70                        75

Ile Leu Pro Glu His Leu Lys Glu Phe Gln Ser Leu Glu Thr Leu  
                  80                        85                        90

Asp Leu Ser Ser Asn Asn Ile Ser Glu Leu Gln Thr Ala Phe Pro  
                  95                        100                      105

Ala Leu Gln Leu Lys Tyr Leu Tyr Leu Asn Ser Asn Arg Val Thr  
                  110                       115                      120

Ser Met Glu Pro Gly Tyr Phe Asp Asn Leu Ala Asn Thr Leu Leu  
                  125                       130                      135

Val Leu Lys Leu Asn Arg Asn Arg Ile Ser Ala Ile Pro Pro Lys  
                  140                       145                      150

Met Phe Lys Leu Pro Gln Leu Gln His Leu Glu Leu Asn Arg Asn  
                  155                       160                      165

Lys Ile Lys Asn Val Asp Gly Leu Thr Phe Gln Gly Leu Gly Ala  
                  170                       175                      180

Leu Lys Ser Leu Lys Met Gln Arg Asn Gly Val Thr Lys Leu Met  
                  185                       190                      195

Asp Gly Ala Phe Trp Gly Leu Ser Asn Met Glu Ile Leu Gln Leu  
                  200                       205                      210

Asp His Asn Asn Leu Thr Glu Ile Thr Lys Gly Trp Leu Tyr Gly  
                  215                       220                      225

Leu Leu Met Leu Gln Glu Leu His Leu Ser Gln Asn Ala Ile Asn  
                  230                       235                      240

Arg Ile Ser Pro Asp Ala Trp Glu Phe Cys Gln Lys Leu Ser Glu  
                  245                       250                      255

Leu Asp Leu Thr Phe Asn His Leu Ser Arg Leu Asp Asp Ser Ser  
                  260                       265                      270

Phe Leu Gly Leu Ser Leu Leu Asn Thr Leu His Ile Gly Asn Asn  
                  275                       280                      285

Arg Val Ser Tyr Ile Ala Asp Cys Ala Phe Arg Gly Leu Ser Ser

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Leu Lys Thr Leu Asp Leu Lys Asn Asn Glu Ile Ser Trp Thr Ile		
305	310	315
Glu Asp Met Asn Gly Ala Phe Ser Gly Leu Asp Lys Leu Arg Arg		
320	325	330
Leu Ile Leu Gln Gly Asn Arg Ile Arg Ser Ile Thr Lys Lys Ala		
335	340	345
Phe Thr Gly Leu Asp Ala Leu Glu His Leu Asp Leu Ser Asp Asn		
350	355	360
Ala Ile Met Ser Leu Gln Gly Asn Ala Phe Ser Gln Met Lys Lys		
365	370	375
Leu Gln Gln Leu His Leu Asn Thr Ser Ser Leu Leu Cys Asp Cys		
380	385	390
Gln Leu Lys Trp Leu Pro Gln Trp Val Ala Glu Asn Asn Phe Gln		
395	400	405
Ser Phe Val Asn Ala Ser Cys Ala His Pro Gln Leu Leu Lys Gly		
410	415	420
Arg Ser Ile Phe Ala Val Ser Pro Asp Gly Phe Val Cys Asp Asp		
425	430	435
Phe Pro Lys Pro Gln Ile Thr Val Gln Pro Glu Thr Gln Ser Ala		
440	445	450
Ile Lys Gly Ser Asn Leu Ser Phe Ile Cys Ser Ala Ala Ser Ser		
455	460	465
Ser Asp Ser Pro Met Thr Phe Ala Trp Lys Lys Asp Asn Glu Leu		
470	475	480
Leu His Asp Ala Glu Met Glu Asn Tyr Ala His Leu Arg Ala Gln		
485	490	495
Gly Gly Glu Val Met Glu Tyr Thr Thr Ile Leu Arg Leu Arg Glu		
500	505	510
Val Glu Phe Ala Ser Glu Gly Lys Tyr Gln Cys Val Ile Ser Asn		
515	520	525
His Phe Gly Ser Ser Tyr Ser Val Lys Ala Lys Leu Thr Val Asn		
530	535	540
Met Leu Pro Ser Phe Thr Lys Thr Pro Met Asp Leu Thr Ile Arg		
545	550	555

Ala Gly Ala Met Ala Arg Leu Glu Cys Ala Ala Val Gly His Pro  
                   560                  565                  570  
  
 Ala Pro Gln Ile Ala Trp Gln Lys Asp Gly Gly Thr Asp Phe Pro  
                   575                  580                  585  
  
 Ala Ala Arg Glu Arg Arg Met His Val Met Pro Glu Asp Asp Val  
                   590                  595                  600  
  
 Phe Phe Ile Val Asp Val Lys Ile Glu Asp Ile Gly Val Tyr Ser  
                   605                  610                  615  
  
 Cys Thr Ala Gln Asn Ser Ala Gly Ser Ile Ser Ala Asn Ala Thr  
                   620                  625                  630  
  
 Leu Thr Val Leu Glu Thr Pro Ser Phe Leu Arg Pro Leu Leu Asp  
                   635                  640                  645  
  
 Arg Thr Val Thr Lys Gly Glu Thr Ala Val Leu Gln Cys Ile Ala  
                   650                  655                  660  
  
 Gly Gly Ser Pro Pro Pro Lys Leu Asn Trp Thr Lys Asp Asp Ser  
                   665                  670                  675  
  
 Pro Leu Val Val Thr Glu Arg His Phe Phe Ala Ala Gly Asn Gln  
                   680                  685                  690  
  
 Leu Leu Ile Ile Val Asp Ser Asp Val Ser Asp Ala Gly Lys Tyr  
                   695                  700                  705  
  
 Thr Cys Glu Met Ser Asn Thr Leu Gly Thr Glu Arg Gly Asn Val  
                   710                  715                  720  
  
 Arg Leu Ser Val Ile Pro Thr Pro Thr Cys Asp Ser Pro Gln Met  
                   725                  730                  735  
  
 Thr Ala Pro Ser Leu Asp Asp Asp Gly Trp Ala Thr Val Gly Val  
                   740                  745                  750  
  
 Val Ile Ile Ala Val Val Cys Cys Val Val Gly Thr Ser Leu Val  
                   755                  760                  765  
  
 Trp Val Val Ile Ile Tyr His Thr Arg Arg Asn Glu Asp Cys  
                   770                  775                  780  
  
 Ser Ile Thr Asn Thr Asp Glu Thr Asn Leu Pro Ala Asp Ile Pro  
                   785                  790                  795  
  
 Ser Tyr Leu Ser Ser Gln Gly Thr Leu Ala Asp Arg Gln Asp Gly  
                   800                  805                  810

Tyr Val Ser Ser Glu Ser Gly Ser His His Gln Phe Val Thr Ser  
 815 820 825  
 Ser Gly Ala Gly Phe Phe Leu Pro Gln His Asp Ser Ser Gly Thr  
 830 835 840  
 Cys His Ile Asp Asn Ser Ser Glu Ala Asp Val Glu Ala Ala Thr  
 845 850 855  
 Asp Leu Phe Leu Cys Pro Phe Leu Gly Ser Thr Gly Pro Met Tyr  
 860 865 870  
 Leu Lys Gly Asn Val Tyr Gly Ser Asp Pro Phe Glu Thr Tyr His  
 875 880 885  
 Thr Gly Cys Ser Pro Asp Pro Arg Thr Val Leu Met Asp His Tyr  
 890 895 900  
 Glu Pro Ser Tyr Ile Lys Lys Lys Glu Cys Tyr Pro Cys Ser His  
 905 910 915  
 Pro Ser Glu Glu Ser Cys Glu Arg Ser Phe Ser Asn Ile Ser Trp  
 920 925 930  
 Pro Ser His Val Arg Lys Leu Leu Asn Thr Ser Tyr Ser His Asn  
 935 940 945  
 Glu Gly Pro Gly Met Lys Asn Leu Cys Leu Asn Lys Ser Ser Leu  
 950 955 960  
 Asp Phe Ser Ala Asn Pro Glu Pro Ala Ser Val Ala Ser Ser Asn  
 965 970 975  
 Ser Phe Met Gly Thr Phe Gly Lys Ala Leu Arg Arg Pro His Leu  
 980 985 990  
 Asp Ala Tyr Ser Ser Phe Gly Gln Pro Ser Asp Cys Gln Pro Arg  
 995 1000 1005  
 Ala Phe Tyr Leu Lys Ala His Ser Ser Pro Asp Leu Asp Ser Gly  
 1010 1015 1020  
 Ser Glu Glu Asp Gly Lys Glu Arg Thr Asp Phe Gln Glu Glu Asn  
 1025 1030 1035  
 His Ile Cys Thr Phe Lys Gln Thr Leu Glu Asn Tyr Arg Thr Pro  
 1040 1045 1050  
 Asn Phe Gln Ser Tyr Asp Leu Asp Thr  
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&lt;210&gt; 291

&lt;211&gt; 2906

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;400&gt; 291

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GGTGTGGTGG TGTTTCCTT TCCTTTGAA TTTCCACAA GAGGAGAGGA 500  
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GCAGATTGAG GCATTGATTG GGGGAGAGAA ACCAGCAGAG CACAGTTGGA 600  
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TTCATCAACC TCCTTTTTT TAAATTTTA TTCCTTTGG TATCAAGATC 700  
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 caaaaa 2906

&lt;210&gt; 292

&lt;211&gt; 640

&lt;212&gt; PRT

&lt;213&gt; Homo Sapien

&lt;400&gt; 292

Met	Leu	Asn	Lys	Met	Thr	Leu	His	Pro	Gln	Gln	Ile	Met	Ile	Gly
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Pro	Arg	Phe	Asn	Arg	Ala	Leu	Phe	Asp	Pro	Leu	Leu	Val	Val	Leu
					20				25			30		
Leu	Ala	Leu	Gln	Leu	Leu	Val	Val	Ala	Gly	Leu	Val	Arg	Ala	Gln
					35				40			45		
Thr	Cys	Pro	Ser	Val	Cys	Ser	Cys	Ser	Asn	Gln	Phe	Ser	Lys	Val
					50				55			60		
Ile	Cys	Val	Arg	Lys	Asn	Leu	Arg	Glu	Val	Pro	Asp	Gly	Ile	Ser
					65				70			75		
Thr	Asn	Thr	Arg	Leu	Leu	Asn	Leu	His	Glu	Asn	Gln	Ile	Gln	Ile
					80				85			90		
Ile	Lys	Val	Asn	Ser	Phe	Lys	His	Leu	Arg	His	Leu	Glu	Ile	Leu
					95				100			105		
Gln	Leu	Ser	Arg	Asn	His	Ile	Arg	Thr	Ile	Glu	Ile	Gly	Ala	Phe
					110				115			120		
Asn	Gly	Leu	Ala	Asn	Leu	Asn	Thr	Leu	Glu	Leu	Phe	Asp	Asn	Arg
					125				130			135		
Leu	Thr	Thr	Ile	Pro	Asn	Gly	Ala	Phe	Val	Tyr	Leu	Ser	Lys	Leu
					140				145			150		
Lys	Glu	Leu	Trp	Leu	Arg	Asn	Asn	Pro	Ile	Glu	Ser	Ile	Pro	Ser

155	160	165
Tyr Ala Phe Asn Arg Ile Pro Ser Leu Arg Arg Leu Asp Leu Gly 170	175	180
Glu Leu Lys Arg Leu Ser Tyr Ile Ser Glu Gly Ala Phe Glu Gly 185	190	195
Leu Ser Asn Leu Arg Tyr Leu Asn Leu Ala Met Cys Asn Leu Arg 200	205	210
Glu Ile Pro Asn Leu Thr Pro Leu Ile Lys Leu Asp Glu Leu Asp 215	220	225
Leu Ser Gly Asn His Leu Ser Ala Ile Arg Pro Gly Ser Phe Gln 230	235	240
Gly Leu Met His Leu Gln Lys Leu Trp Met Ile Gln Ser Gln Ile 245	250	255
Gln Val Ile Glu Arg Asn Ala Phe Asp Asn Leu Gln Ser Leu Val 260	265	270
Glu Ile Asn Leu Ala His Asn Asn Leu Thr Leu Leu Pro His Asp 275	280	285
Leu Phe Thr Pro Leu His His Leu Glu Arg Ile His Leu His His 290	295	300
Asn Pro Trp Asn Cys Asn Cys Asp Ile Leu Trp Leu Ser Trp Trp 305	310	315
Ile Lys Asp Met Ala Pro Ser Asn Thr Ala Cys Cys Ala Arg Cys 320	325	330
Asn Thr Pro Pro Asn Leu Lys Gly Arg Tyr Ile Gly Glu Leu Asp 335	340	345
Gln Asn Tyr Phe Thr Cys Tyr Ala Pro Val Ile Val Glu Pro Pro 350	355	360
Ala Asp Leu Asn Val Thr Glu Gly Met Ala Ala Glu Leu Lys Cys 365	370	375
Arg Ala Ser Thr Ser Leu Thr Ser Val Ser Trp Ile Thr Pro Asn 380	385	390
Gly Thr Val Met Thr His Gly Ala Tyr Lys Val Arg Ile Ala Val 395	400	405
Leu Ser Asp Gly Thr Leu Asn Phe Thr Asn Val Thr Val Gln Asp 410	415	420

Thr Gly Met Tyr Thr Cys Met Val Ser Asn Ser Val Gly Asn Thr  
                   425                  430                  435  
 Thr Ala Ser Ala Thr Leu Asn Val Thr Ala Ala Thr Thr Thr Pro  
                   440                  445                  450  
 Phe Ser Tyr Phe Ser Thr Val Thr Val Glu Thr Met Glu Pro Ser  
                   455                  460                  465  
 Gln Asp Glu Ala Arg Thr Thr Asp Asn Asn Val Gly Pro Thr Pro  
                   470                  475                  480  
 Val Val Asp Trp Glu Thr Thr Asn Val Thr Thr Ser Leu Thr Pro  
                   485                  490                  495  
 Gln Ser Thr Arg Ser Thr Glu Lys Thr Phe Thr Ile Pro Val Thr  
                   500                  505                  510  
 Asp Ile Asn Ser Gly Ile Pro Gly Ile Asp Glu Val Met Lys Thr  
                   515                  520                  525  
 Thr Lys Ile Ile Ile Gly Cys Phe Val Ala Ile Thr Leu Met Ala  
                   530                  535                  540  
 Ala Val Met Leu Val Ile Phe Tyr Lys Met Arg Lys Gln His His  
                   545                  550                  555  
 Arg Gln Asn His His Ala Pro Thr Arg Thr Val Glu Ile Ile Asn  
                   560                  565                  570  
 Val Asp Asp Glu Ile Thr Gly Asp Thr Pro Met Glu Ser His Leu  
                   575                  580                  585  
 Pro Met Pro Ala Ile Glu His Glu His Leu Asn His Tyr Asn Ser  
                   590                  595                  600  
 Tyr Lys Ser Pro Phe Asn His Thr Thr Val Asn Thr Ile Asn  
                   605                  610                  615  
 Ser Ile His Ser Ser Val His Glu Pro Leu Leu Ile Arg Met Asn  
                   620                  625                  630  
 Ser Lys Asp Asn Val Gln Glu Thr Gln Ile  
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 cccgagccac tcccgtcctg ggtcgctcgg ctggacttaa gtcacaacag 500  
 attatcttc atcaaggcaa gttccatgag ccaccccaa agccttcgag 550  
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Pro Cys Pro Thr Thr Cys Arg Cys Leu Gly Asp Leu Leu Asp Cys  
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Ser Arg Lys Arg Leu Ala Arg Leu Pro Glu Pro Leu Pro Ser Trp  
65 70 75

Val Ala Arg Leu Asp Leu Ser His Asn Arg Leu Ser Phe Ile Lys  
80 85 90

Ala Ser Ser Met Ser His Leu Gln Ser Leu Arg Glu Val Lys Leu  
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Ile Leu Pro Glu His Leu Lys Glu Phe Gln Ser Leu Glu Thr Leu  
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Ser Met Glu Pro Gly Tyr Phe Asp Asn Leu Ala Asn Thr Leu Leu  
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Val Leu Lys Leu Asn Arg Asn Arg Ile Ser Ala Ile Pro Pro Lys  
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Met Phe Lys Leu Pro Gln Leu Gln His Leu Glu Leu Asn Arg Asn

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Leu Leu Met Leu Gln Glu Leu His Leu Ser Gln Asn Ala Ile Asn		
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Phe Leu Gly Leu Ser Leu Leu Asn Thr Leu His Ile Gly Asn Asn		
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Phe Thr Gly Leu Asp Ala Leu Glu His Leu Asp Leu Ser Asp Asn		
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455	460	465
Ser Phe Val Asn Ala Ser Cys Ala His Pro Gln Leu Leu Lys Gly		
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 830 835 840

Ser Ile Thr Asn Thr Asp Glu Thr Asn Leu Pro Ala Asp Ile Pro  
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Cys His Ile Asp Asn Ser Ser Glu Ala Asp Val Glu Ala Ala Thr  
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 950 955 960

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 980 985 990

Pro Ser His Val Arg Lys Leu Leu Asn Thr Ser Tyr Ser His Asn  
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 aaaaacctgt aatcaagatc taaatgagtg tggcctgaag ccccgccct 500  
 gtaaggcacag gtgc当地 gacttacggca gctacaagtg ctactgtctc 550  
 aacggatata tgctcatgcc ggatgggttcc tgctcaagtg ccctgacctg 600  
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 ggtgccagtg cccatccc当地 ggctgc当地 tggctctga tgggaggacc 700  
 tgtgttagatg ttgatgaatg tgctacagga agagcctctt gccctagatt 750  
 taggcaatgt gtcaacactt ttgggagcta catctgc当地 tgc当地 800  
 gcttc当地 catgtatatt ggaggcaat atcaatgtca tgacatagac 850  
 gaatgctcac ttggtagta tcagtgccagc agctttgctc gatgttataa 900  
 cgtacgtggg tcctacaagt gcaaata gaaaggatac cagggtgatg 950  
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 catcttgaaa attatttaat gtttctaaa ataaaaaatg ttagtggttt 2950  
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 aat 3003

<210> 315  
 <211> 509  
 <212> PRT  
 <213> Homo Sapien

<400> 315  
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 Gln Ala Ala Ala Glu Phe Asp Gly Arg Trp Pro Arg Gln Ile Val  
 20 25 30  
 Ser Ser Ile Gly Leu Cys Arg Tyr Gly Gly Arg Ile Asp Cys Cys  
 35 40 45  
 Trp Gly Trp Ala Arg Gln Ser Trp Gly Gln Cys Gln Pro Val Cys  
 50 55 60  
 Gln Pro Arg Cys Lys His Gly Glu Cys Ile Gly Pro Asn Lys Cys  
 65 70 75  
 Lys Cys His Pro Gly Tyr Ala Gly Lys Thr Cys Asn Gln Asp Leu  
 80 85 90  
 Asn Glu Cys Gly Leu Lys Pro Arg Pro Cys Lys His Arg Cys Met  
 95 100 105  
 Asn Thr Tyr Gly Ser Tyr Lys Cys Tyr Cys Leu Asn Gly Tyr Met  
 110 115 120  
 Leu Met Pro Asp Gly Ser Cys Ser Ser Ala Leu Thr Cys Ser Met  
 125 130 135  
 Ala Asn Cys Gln Tyr Gly Cys Asp Val Val Lys Gly Gln Ile Arg  
 140 145 150  
 Cys Gln Cys Pro Ser Pro Gly Leu His Leu Ala Pro Asp Gly Arg  
 155 160 165

Thr Cys Val Asp Val Asp Glu Cys Ala Thr Gly Arg Ala Ser Cys  
 170 175 180  
 Pro Arg Phe Arg Gln Cys Val Asn Thr Phe Gly Ser Tyr Ile Cys  
 185 190 195  
 Lys Cys His Lys Gly Phe Asp Leu Met Tyr Ile Gly Gly Lys Tyr  
 200 205 210  
 Gln Cys His Asp Ile Asp Glu Cys Ser Leu Gly Gln Tyr Gln Cys  
 215 220 225  
 Ser Ser Phe Ala Arg Cys Tyr Asn Val Arg Gly Ser Tyr Lys Cys  
 230 235 240  
 Lys Cys Lys Glu Gly Tyr Gln Gly Asp Gly Leu Thr Cys Val Tyr  
 245 250 255  
 Ile Pro Lys Val Met Ile Glu Pro Ser Gly Pro Ile His Val Pro  
 260 265 270  
 Lys Gly Asn Gly Thr Ile Leu Lys Gly Asp Thr Gly Asn Asn Asn  
 275 280 285  
 Trp Ile Pro Asp Val Gly Ser Thr Trp Trp Pro Pro Lys Thr Pro  
 290 295 300  
 Tyr Ile Pro Pro Ile Ile Thr Asn Arg Pro Thr Ser Lys Pro Thr  
 305 310 315  
 Thr Arg Pro Thr Pro Lys Pro Thr Pro Ile Pro Thr Pro Pro Pro  
 320 325 330  
 Pro Pro Pro Leu Pro Thr Glu Leu Arg Thr Pro Leu Pro Pro Thr  
 335 340 345  
 Thr Pro Glu Arg Pro Thr Thr Gly Leu Thr Thr Ile Ala Pro Ala  
 350 355 360  
 Ala Ser Thr Pro Pro Gly Gly Ile Thr Val Asp Asn Arg Val Gln  
 365 370 375  
 Thr Asp Pro Gln Lys Pro Arg Gly Asp Val Phe Ser Val Leu Val  
 380 385 390  
 His Ser Cys Asn Phe Asp His Gly Leu Cys Gly Trp Ile Arg Glu  
 395 400 405  
 Lys Asp Asn Asp Leu His Trp Glu Pro Ile Arg Asp Pro Ala Gly  
 410 415 420  
 Gly Gln Tyr Leu Thr Val Ser Ala Ala Lys Ala Pro Gly Gly Lys

425	430	435
Ala Ala Arg Leu Val Leu Pro Leu Gly Arg Leu Met His Ser Gly		
440	445	450
Asp Leu Cys Leu Ser Phe Arg His Lys Val Thr Gly Leu His Ser		
455	460	465
Gly Thr Leu Gln Val Phe Val Arg Lys His Gly Ala His Gly Ala		
470	475	480
Ala Leu Trp Gly Arg Asn Gly Gly His Gly Trp Arg Gln Thr Gln		
485	490	495
Ile Thr Leu Arg Gly Ala Asp Ile Lys Ser Glu Ser Gln Arg		
500	505	

<210> 316  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 316  
gatggttcct gctcaagtgc cctg 24

<210> 317  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 317  
ttgcacttgt aggaccacg tacg 24

<210> 318  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 318  
ctgatggag gacctgtgt aatgtgctac aggaagagcc 50

<210> 319  
<211> 2110  
<212> DNA

<213> Homo Sapien

<400> 319  
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tttagattgt gaaatgtggc tcaaggtctt cacaacttc cttcc 100  
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catggcgtca gaggtcaggc cctctaccta cccgtccact atggcttcca 200  
caactccagca tcagacatcc agatcatatg gctatttgag agaccccaca 250  
caatgccccaa atacttactg ggctctgtga ataagtctgt ggtcctgac 300  
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gttcatgtatc ctgtcacaaa gccagtggtg cagattcatc ctccctctgg 500  
ggctgtggag tatgtggggaa acatgaccct gacatgccat gtggaaagg 550  
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agtaaccaag gaagacattt ggaattacag ctgcctggtg aggaaccctg 700  
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atccccccaa cacctactcc tggatttagga ggactgacaa tactacatata 900  
atcattaagc atgggcctcg cttagaagtt gcatctgaga aagtagcccc 950  
gaagacaatg gactatgtgt gctgtgctt caacaacata accggcaggc 1000  
aagatgaaac tcatttcaca gttatcatca cttccgtagg actggagaag 1050  
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atcactatcc ttgatttatccatgtgtct tctcttcata tggaaaaaat 1150  
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 aatcagtgaa gaaaccagga ccaacacctc ttactcatta ttcctttaca 1550  
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 ttctatctt acattttgtac aacaaagtaa taaggatggt tgtcacaaaa 1950  
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 agacttgta acacttaagg aaatgactat taaagtctt ttttatttt 2050  
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 aaaaaaaaaa 2110

<210> 320  
 <211> 450  
 <212> PRT  
 <213> Homo Sapien

<400> 320			
Met Trp Leu Lys Val Phe Thr Thr Phe Leu Ser Phe Ala Thr Gly			
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20	25	30	
Gly Val Arg Gly Gln Ala Leu Tyr Leu Pro Val His Tyr Gly Phe			
35	40	45	
His Thr Pro Ala Ser Asp Ile Gln Ile Ile Trp Leu Phe Glu Arg			
50	55	60	

Pro His Thr Met Pro Lys Tyr Leu Leu Gly Ser Val Asn Lys Ser  
       65                    70                    75  
 Val Val Pro Asp Leu Glu Tyr Gln His Lys Phe Thr Met Met Pro  
       80                    85                    90  
 Pro Asn Ala Ser Leu Leu Ile Asn Pro Leu Gln Phe Pro Asp Glu  
       95                    100                   105  
 Gly Asn Tyr Ile Val Lys Val Asn Ile Gln Gly Asn Gly Thr Leu  
       110                   115                   120  
 Ser Ala Ser Gln Lys Ile Gln Val Thr Val Asp Asp Pro Val Thr  
       125                   130                   135  
 Lys Pro Val Val Gln Ile His Pro Pro Ser Gly Ala Val Glu Tyr  
       140                   145                   150  
 Val Gly Asn Met Thr Leu Thr Cys His Val Glu Gly Gly Thr Arg  
       155                   160                   165  
 Leu Ala Tyr Gln Trp Leu Lys Asn Gly Arg Pro Val His Thr Ser  
       170                   175                   180  
 Ser Thr Tyr Ser Phe Ser Pro Gln Asn Asn Thr Leu His Ile Ala  
       185                   190                   195  
 Pro Val Thr Lys Glu Asp Ile Gly Asn Tyr Ser Cys Leu Val Arg  
       200                   205                   210  
 Asn Pro Val Ser Glu Met Glu Ser Asp Ile Ile Met Pro Ile Ile  
       215                   220                   225  
 Tyr Tyr Gly Pro Tyr Gly Leu Gln Val Asn Ser Asp Lys Gly Leu  
       230                   235                   240  
 Lys Val Gly Glu Val Phe Thr Val Asp Leu Gly Glu Ala Ile Leu  
       245                   250                   255  
 Phe Asp Cys Ser Ala Asp Ser His Pro Pro Asn Thr Tyr Ser Trp  
       260                   265                   270  
 Ile Arg Arg Thr Asp Asn Thr Thr Tyr Ile Ile Lys His Gly Pro  
       275                   280                   285  
 Arg Leu Glu Val Ala Ser Glu Lys Val Ala Gln Lys Thr Met Asp  
       290                   295                   300  
 Tyr Val Cys Cys Ala Tyr Asn Asn Ile Thr Gly Arg Gln Asp Glu  
       305                   310                   315  
 Thr His Phe Thr Val Ile Ile Thr Ser Val Gly Leu Glu Lys Leu

320	325	330
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Ala Gln Lys Gly Lys Ser Leu Ser Pro Leu Ala Ser Ile Thr Gly	340	345
335		

Ile Ser Leu Phe Leu Ile Ile Ser Met Cys Leu Leu Phe Leu Trp	355	360
350		

Lys Lys Tyr Gln Pro Tyr Lys Val Ile Lys Gln Lys Leu Glu Gly	370	375
365		

Arg Pro Glu Thr Glu Tyr Arg Lys Ala Gln Thr Phe Ser Gly His	385	390
380		

Glu Asp Ala Leu Asp Asp Phe Gly Ile Tyr Glu Phe Val Ala Phe	400	405
395		

Pro Asp Val Ser Gly Val Ser Arg Ile Pro Ser Arg Ser Val Pro	415	420
410		

Ala Ser Asp Cys Val Ser Gly Gln Asp Leu His Ser Thr Val Tyr.	430	435
425		

Glu Val Ile Gln His Ile Pro Ala Gln Gln Gln Asp His Pro Glu	445	450
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<210> 321

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 321

gatcctgtca caaagccagt ggtgc 25

<210> 322

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 322

cactgacagg gttcctcacc cagg 24

<210> 323

<211> 45

<212> DNA

<213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 323

ctccctctgg gctgtggagt atgtgggaa catgaccctg acatg 45

&lt;210&gt; 324

&lt;211&gt; 2397

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;400&gt; 324

gcaagcggcg aaatggcgcc ctccgggagt cttgcagttc ccctggcagt 50

cctggtgctg ttgcttggg gtgctccctg gacgcacggg cggcggagca 100

acgttcgcgt catcacggac gagaactgga gagaactgct ggaaggagac 150

tggatgatag aatttatgc cccgtggtgc cctgcttgc aaaatcttca 200

accggaatgg gaaagtttg ctgaatgggg agaagatctt gaggttaata 250

ttgcgaaagt agatgtcaca gaggcagccag gactgagtgg acggtttatac 300

ataactgctc ttccctactat ttatcattgt aaagatggtg aatttaggcg 350

ctatcagggt ccaaggacta agaaggactt cataaacttt ataagtgata 400

aagagtggaa gagtattgag cccgtttcat catggttgg tccaggttct 450

gttctgatga gtagtatgtc agcactctt cagctatcta tgtggatcag 500

gacgtgccat aactactta ttgaagacct tggattgcca gtgtgggat 550

catatactgt ttttgctta gcaactctgt tttccggact gttattagga 600

ctctgtatga tatttgtggc agattgcctt tgcccttcaa aaaggcgcag 650

accacagcca tacccatacc cttcaaaaaa attattatca gaatctgcac 700

aacctttgaa aaaagtggag gaggaacaag aggccgatga agaagatgtt 750

tcagaagaag aagctgaaag taaagaagga acaaacaag actttccaca 800

gaatgccata agacaacgct ctctgggtcc atcattggcc acagataaat 850

cctagttaaa ttttatagtt atcttaatat tatgattttg ataaaaacag 900

aagattgatc attttgggg gtttgaagtg aactgtgact tttttgaata 950

ttgcagggtt cagtctagat tgcattaaa ttgaagagtc tacattcaga 1000

acataaaagc actaggata caagttgaa atatgattt agcacagtat 1050  
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atttatgtat atttgtaa taataaccta tttcaagtct gagttttgaa 1150  
aatttacatt tcccaagtat tgcattattt aggtatttaa gaagattt 1200  
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tctgttgctg tgtgaatcca ttagatttac agtacgtaa tatacaagtt 2250  
ttctttaaag ccctctccctt tagaatttaa aatattgtac cattaaagag 2300  
tttggatgtg taacttgtga tgccttagaa aaatatccta agcacaaaat 2350

aaacctttct aaccacctca ttaaagctga aaaaaaaaaa aaaaaaaa 2397

<210> 325  
<211> 280  
<212> PRT

<213> Homo Sapien

<400> 325

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20 25 30														
Val Arg Val Ile Thr Asp Glu Asn Trp Arg Glu Leu Leu Glu Gly														
35 40 45														
Asp Trp Met Ile Glu Phe Tyr Ala Pro Trp Cys Pro Ala Cys Gln														
50 55 60														
Asn Leu Gln Pro Glu Trp Glu Ser Phe Ala Glu Trp Gly Glu Asp														
65 70 75														
Leu Glu Val Asn Ile Ala Lys Val Asp Val Thr Glu Gln Pro Gly														
80 85 90														
Leu Ser Gly Arg Phe Ile Ile Thr Ala Leu Pro Thr Ile Tyr His														
95 100 105														
Cys Lys Asp Gly Glu Phe Arg Arg Tyr Gln Gly Pro Arg Thr Lys														
110 115 120														
Lys Asp Phe Ile Asn Phe Ile Ser Asp Lys Glu Trp Lys Ser Ile														
125 130 135														
Glu Pro Val Ser Ser Trp Phe Gly Pro Gly Ser Val Leu Met Ser														
140 145 150														
Ser Met Ser Ala Leu Phe Gln Leu Ser Met Trp Ile Arg Thr Cys														
155 160 165														
His Asn Tyr Phe Ile Glu Asp Leu Gly Leu Pro Val Trp Gly Ser														
170 175 180														
Tyr Thr Val Phe Ala Leu Ala Thr Leu Phe Ser Gly Leu Leu Leu														
185 190 195														
Gly Leu Cys Met Ile Phe Val Ala Asp Cys Leu Cys Pro Ser Lys														
200 205 210														
Arg Arg Arg Pro Gln Pro Tyr Pro Tyr Pro Ser Lys Lys Leu Leu														

215

220

225

Ser Glu Ser Ala Gln Pro Leu Lys Lys Val Glu Glu Glu Gln Glu  
230 235 240

Ala Asp Glu Glu Asp Val Ser Glu Glu Ala Glu Ser Lys Glu  
245 250 255

Gly Thr Asn Lys Asp Phe Pro Gln Asn Ala Ile Arg Gln Arg Ser  
260 265 270

Leu Gly Pro Ser Leu Ala Thr Asp Lys Ser  
275 280

<210> 326

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 326

ttaggtgggc aagcggcgaa atg 23

<210> 327

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 327

tatgtggatc aggacgtgcc 20

<210> 328

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 328

tgcagggttc agtctagatt g 21

<210> 329

<211> 25

<212> DNA

<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe  
  
<400> 329  
ttgaaggaca aaggcaatct gccac 25  
  
<210> 330  
<211> 45  
<212> DNA  
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<223> Synthetic Oligonucleotide Probe  
  
<400> 330  
ggagtcttgc agttcccttg gcagtcctgg tgctgttgct ttggg 45  
  
<210> 331  
<211> 2168  
<212> DNA  
<213> Homo Sapien  
  
<400> 331  
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aacgggaccc ttctgtgtgc cagaaaccgc aagcagttgc taacccagtg 100  
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acttccctct gtgaccatga aactctgggt gtctgcattg ctgatggcct 200  
ggtttggtgt cctgagctgt gtgcaggccg aattttcac ctctattggg 250  
cacatgactg acctgattta tgcagagaaa gagctggtgc agtctctgaa 300  
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caatgctgag tgtggatgac tgctttggga tggccgctc ggcctacaat 700  
gaaggggact attatcatac ggtgttggg atggagcagg tgctaaagca 750

gcttgatgcc ggggaggagg ccaccacaac caagtcacag gtgctggact 800  
 acctcagcta tgctgtctc cagttgggtg atctgcaccc tgccctggag 850  
 ctcacccgcc gcctgctctc ccttgaccca agccacgaac gagctggagg 900  
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 ctgcagaatt gttacaggtt gcaaattatg gagtgggagg acagtatgaa 1450  
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 gtttagctgtc tagcgcttag caaggtgcct ttgtacctca ggtgttttag 2050  
 gtgtgagatg tttcagtgaa ccaaagttct gataccttgtt ttacatgttt 2100

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<210> 332  
 <211> 533  
 <212> PRT  
 <213> Homo Sapien

<400> 332  
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Leu Ser Cys Val Gln Ala Glu Phe Phe Thr Ser Ile Gly His Met  
       20                       25                       30

Thr Asp Leu Ile Tyr Ala Glu Glu Leu Val Gln Ser Leu Lys  
       35                       40                       45

Glu Tyr Ile Leu Val Glu Glu Ala Lys Leu Ser Lys Ile Lys Ser  
       50                       55                       60

Trp Ala Asn Lys Met Glu Ala Leu Thr Ser Lys Ser Ala Ala Asp  
       65                       70                       75

Ala Glu Gly Tyr Leu Ala His Pro Val Asn Ala Tyr Lys Leu Val  
       80                       85                       90

Lys Arg Leu Asn Thr Asp Trp Pro Ala Leu Glu Asp Leu Val Leu  
       95                       100                       105

Gln Asp Ser Ala Ala Gly Phe Ile Ala Asn Leu Ser Val Gln Arg  
       110                       115                       120

Gln Phe Phe Pro Thr Asp Glu Asp Glu Ile Gly Ala Ala Lys Ala  
       125                       130                       135

Leu Met Arg Leu Gln Asp Thr Tyr Arg Leu Asp Pro Gly Thr Ile  
       140                       145                       150

Ser Arg Gly Glu Leu Pro Gly Thr Lys Tyr Gln Ala Met Leu Ser  
       155                       160                       165

Val Asp Asp Cys Phe Gly Met Gly Arg Ser Ala Tyr Asn Glu Gly  
       170                       175                       180

Asp Tyr Tyr His Thr Val Leu Trp Met Glu Gln Val Leu Lys Gln  
       185                       190                       195

Leu Asp Ala Gly Glu Glu Ala Thr Thr Lys Ser Gln Val Leu  
       200                       205                       210

Asp Tyr Leu Ser Tyr Ala Val Phe Gln Leu Gly Asp Leu His Arg  
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 Ala Leu Glu Leu Thr Arg Arg Leu Leu Ser Leu Asp Pro Ser His  
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 Glu Arg Ala Gly Gly Asn Leu Arg Tyr Phe Glu Gln Leu Leu Glu  
                   245                  250                  255  
  
 Glu Glu Arg Glu Lys Thr Leu Thr Asn Gln Thr Glu Ala Glu Leu  
                   260                  265                  270  
  
 Ala Thr Pro Glu Gly Ile Tyr Glu Arg Pro Val Asp Tyr Leu Pro  
                   275                  280                  285  
  
 Glu Arg Asp Val Tyr Glu Ser Leu Cys Arg Gly Glu Gly Val Lys  
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                   305                  310                  315  
  
 Gly Asn Arg Ala Pro Gln Leu Leu Ile Ala Pro Phe Lys Glu Glu  
                   320                  325                  330  
  
 Asp Glu Trp Asp Ser Pro His Ile Val Arg Tyr Tyr Asp Val Met  
                   335                  340                  345  
  
 Ser Asp Glu Glu Ile Glu Arg Ile Lys Glu Ile Ala Lys Pro Lys  
                   350                  355                  360  
  
 Leu Ala Arg Ala Thr Val Arg Asp Pro Lys Thr Gly Val Leu Thr  
                   365                  370                  375  
  
 Val Ala Ser Tyr Arg Val Ser Lys Ser Ser Trp Leu Glu Glu Asp  
                   380                  385                  390  
  
 Asp Asp Pro Val Val Ala Arg Val Asn Arg Arg Met Gln His Ile  
                   395                  400                  405  
  
 Thr Gly Leu Thr Val Lys Thr Ala Glu Leu Leu Gln Val Ala Asn  
                   410                  415                  420  
  
 Tyr Gly Val Gly Gly Gln Tyr Glu Pro His Phe Asp Phe Ser Arg  
                   425                  430                  435  
  
 Arg Pro Phe Asp Ser Gly Leu Lys Thr Glu Gly Asn Arg Leu Ala  
                   440                  445                  450  
  
 Thr Phe Leu Asn Tyr Met Ser Asp Val Glu Ala Gly Gly Ala Thr  
                   455                  460                  465  
  
 Val Phe Pro Asp Leu Gly Ala Ala Ile Trp Pro Lys Lys Gly Thr  
                   470                  475                  480

Ala Val Phe Trp Tyr Asn Leu Leu Arg Ser Gly Glu Gly Asp Tyr  
485 490 495

Arg Thr Arg His Ala Ala Cys Pro Val Leu Val Gly Cys Lys Trp  
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Val Ser Asn Lys Trp Phe His Glu Arg Gly Gln Glu Phe Leu Arg  
515 520 525

Pro Cys Gly Ser Thr Glu Val Asp  
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<210> 333

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 333

ccaggcacaa tttccaga 18

<210> 334

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 334

ggacccttct gtgtgccag 19

<210> 335

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 335

ggtctcaaga actcctgtc 19

<210> 336

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 336  
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 <210> 337  
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 <210> 338  
 <211> 2789  
  
 <212> DNA  
 <213> Homo Sapien  
  
 <400> 338  
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 ggttagttcc gacaccccca cagttggaaaga gcaggcagaa ggagttgtga 150  
 agacaggaca atcttcttgg ggatgctggt cctggaaagcc agcgggcctt 200  
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 cctggggcac ccacccggca gggccctacca ccatgcgact gagctccctg 350  
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 gtgcagcctg agcctcctgc gggtttccctg gatccagggg gagggagaag 450  
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<210> 339  
<211> 772  
<212> PRT  
<213> Homo Sapien

<400> 339

Met	Arg	Leu	Ser	Ser	Leu	Leu	Ala	Leu	Leu	Arg	Pro	Ala	Leu	Pro
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Leu	Ile	Leu	Gly	Leu	Ser	Leu	Gly	Cys	Ser	Leu	Ser	Leu	Leu	Arg
										20			25	30

Val	Ser	Trp	Ile	Gln	Gly	Glu	Gly	Glu	Asp	Pro	Cys	Val	Glu	Ala
										35		40		45

Val	Gly	Glu	Arg	Gly	Gly	Pro	Gln	Asn	Pro	Asp	Ser	Arg	Ala	Arg
										50		55		60

Leu	Asp	Gln	Ser	Asp	Glu	Asp	Phe	Lys	Pro	Arg	Ile	Val	Pro	Tyr
										65		70		75

Tyr	Arg	Asp	Pro	Asn	Lys	Pro	Tyr	Lys	Lys	Val	Leu	Arg	Thr	Arg
										80		85		90

Tyr	Ile	Gln	Thr	Glu	Leu	Gly	Ser	Arg	Glu	Arg	Leu	Leu	Val	Ala
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

95	100	105
Val Leu Thr Ser Arg Ala Thr Leu Ser	Thr Leu Ala Val Ala Val	
110	115	120
Asn Arg Thr Val Ala His His Phe Pro	Arg Leu Leu Tyr Phe Thr	
125	130	135
Gly Gln Arg Gly Ala Arg Ala Pro Ala	Gly Met Gln Val Val Ser	
140	145	150
His Gly Asp Glu Arg Pro Ala Trp	Leu Met Ser Glu Thr Leu Arg	
155	160	165
His Leu His Thr His Phe Gly Ala Asp	Tyr Asp Trp Phe Phe Ile	
170	175	180
Met Gln Asp Asp Thr Tyr Val Gln Ala	Pro Arg Leu Ala Ala Leu	
185	190	195
Ala Gly His Leu Ser Ile Asn Gln Asp	Leu Tyr Leu Gly Arg Ala	
200	205	210
Glu Glu Phe Ile Gly Ala Gly Glu Gln Ala	Arg Tyr Cys His Gly	
215	220	225
Gly Phe Gly Tyr Leu Leu Ser Arg Ser	Leu Leu Leu Arg Leu Arg	
230	235	240
Pro His Leu Asp Gly Cys Arg Gly Asp	Ile Leu Ser Ala Arg Pro	
245	250	255
Asp Glu Trp Leu Gly Arg Cys Leu Ile Asp	Ser Leu Gly Val Gly	
260	265	270
Cys Val Ser Gln His Gln Gly Gln Gln	Tyr Arg Ser Phe Glu Leu	
275	280	285
Ala Lys Asn Arg Asp Pro Glu Lys Glu	Gly Ser Ser Ala Phe Leu	
290	295	300
Ser Ala Phe Ala Val His Pro Val Ser	Glu Gly Thr Leu Met Tyr	
305	310	315
Arg Leu His Lys Arg Phe Ser Ala Leu	Glu Leu Glu Arg Ala Tyr	
320	325	330
Ser Glu Ile Glu Gln Leu Gln Ala Gln	Ile Arg Asn Leu Thr Val	
335	340	345
Leu Thr Pro Glu Gly Glu Ala Gly Leu	Ser Trp Pro Val Gly Leu	
350	355	360

Pro Ala Pro Phe Thr Pro His Ser Arg Phe Glu Val Leu Gly Trp  
                   365                     370                 375  
  
 Asp Tyr Phe Thr Glu Gln His Thr Phe Ser Cys Ala Asp Gly Ala  
                   380                     385                 390  
  
 Pro Lys Cys Pro Leu Gln Gly Ala Ser Arg Ala Asp Val Gly Asp  
                   395                     400                 405  
  
 Ala Leu Glu Thr Ala Leu Glu Gln Leu Asn Arg Arg Tyr Gln Pro  
                   410                     415                 420  
  
 Arg Leu Arg Phe Gln Lys Gln Arg Leu Leu Asn Gly Tyr Arg Arg  
                   425                     430                 435  
  
 Phe Asp Pro Ala Arg Gly Met Glu Tyr Thr Leu Asp Leu Leu Leu  
                   440                     445                 450  
  
 Glu Cys Val Thr Gln Arg Gly His Arg Arg Ala Leu Ala Arg Arg  
                   455                     460                 465  
  
 Val Ser Leu Leu Arg Pro Leu Ser Arg Val Glu Ile Leu Pro Met  
                   470                     475                 480  
  
 Pro Tyr Val Thr Glu Ala Thr Arg Val Gln Leu Val Leu Pro Leu  
                   485                     490                 495  
  
 Leu Val Ala Glu Ala Ala Ala Pro Ala Phe Leu Glu Ala Phe  
                   500                     505                 510  
  
 Ala Ala Asn Val Leu Glu Pro Arg Glu His Ala Leu Leu Thr Leu  
                   515                     520                 525  
  
 Leu Leu Val Tyr Gly Pro Arg Glu Gly Gly Arg Gly Ala Pro Asp  
                   530                     535                 540  
  
 Pro Phe Leu Gly Val Lys Ala Ala Ala Ala Glu Leu Glu Arg Arg  
                   545                     550                 555  
  
 Tyr Pro Gly Thr Arg Leu Ala Trp Leu Ala Val Arg Ala Glu Ala  
                   560                     565                 570  
  
 Pro Ser Gln Val Arg Leu Met Asp Val Val Ser Lys Lys His Pro  
                   575                     580                 585  
  
 Val Asp Thr Leu Phe Phe Leu Thr Thr Val Trp Thr Arg Pro Gly  
                   590                     595                 600  
  
 Pro Glu Val Leu Asn Arg Cys Arg Met Asn Ala Ile Ser Gly Trp  
                   605                     610                 615  
  
 Gln Ala Phe Phe Pro Val His Phe Gln Glu Phe Asn Pro Ala Leu  
                   620                     625                 630

Ser Pro Gln Arg Ser Pro Pro Gly Pro Pro Gly Ala Gly Pro Asp  
 635 640 645  
 Pro Pro Ser Pro Pro Gly Ala Asp Pro Ser Arg Gly Ala Pro Ile  
 650 655 660  
 Gly Gly Arg Phe Asp Arg Gln Ala Ser Ala Glu Gly Cys Phe Tyr  
 665 670 675  
 Asn Ala Asp Tyr Leu Ala Ala Arg Ala Arg Leu Ala Gly Glu Leu  
 680 685 690  
 Ala Gly Gln Glu Glu Glu Ala Leu Glu Gly Leu Glu Val Met  
 695 700 705  
 Asp Val Phe Leu Arg Phe Ser Gly Leu His Leu Phe Arg Ala Val  
 710 715 720  
 Glu Pro Gly Leu Val Gln Lys Phe Ser Leu Arg Asp Cys Ser Pro  
 725 730 735  
 Arg Leu Ser Glu Glu Leu Tyr His Arg Cys Arg Leu Ser Asn Leu  
 740 745 750  
 Glu Gly Leu Gly Gly Arg Ala Gln Leu Ala Met Ala Leu Phe Glu  
 755 760 765  
 Gln Glu Gln Ala Asn Ser Thr  
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 <211> 1572  
 <212> DNA  
 <213> Homo Sapien

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 cttttgaag ggtgtatgc ttggaagcat tttctgtgct ttgatcacta 150  
 tgctaggaca cattaggatt ggtcatggaa atagaatgca ccaccatgag 200  
 catcatcacc tacaagctcc taacaaagaa gatatctga aaatttcaga 250  
 ggatgagcgc atggagctca gtaagagctt tcgagttatac tgtattatcc 300  
 ttgtaaaacc caaagatgtg agtcttggg ctgcagtaaa ggagacttgg 350  
 accaaacact gtgacaaaagc agagttcttc agttctgaaa atgttaaagt 400

gttttagtca attaatatgg acacaaatga catgtggta atgatgagaa 450  
 aagcttacaa atacgcctt gataagtata gagaccaata caactggtc 500  
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<210> 341  
 <211> 318  
 <212> PRT  
 <213> Homo Sapien

<400> 341

Met	Leu	Ser	Glu	Ser	Ser	Ser	Phe	Leu	Lys	Gly	Val	Met	Leu	Gly
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	20							25					30	
Gly	His	Gly	Asn	Arg	Met	His	His	His	Glu	His	His	His	Leu	Gln
	35							40					45	
Ala	Pro	Asn	Lys	Glu	Asp	Ile	Leu	Lys	Ile	Ser	Glu	Asp	Glu	Arg
	50							55					60	
Met	Glu	Leu	Ser	Lys	Ser	Phe	Arg	Val	Tyr	Cys	Ile	Ile	Leu	Val
	65							70					75	
Lys	Pro	Lys	Asp	Val	Ser	Leu	Trp	Ala	Ala	Val	Lys	Glu	Thr	Trp
	80							85					90	
Thr	Lys	His	Cys	Asp	Lys	Ala	Glu	Phe	Phe	Ser	Ser	Glu	Asn	Val
	95							100					105	
Lys	Val	Phe	Glu	Ser	Ile	Asn	Met	Asp	Thr	Asn	Asp	Met	Trp	Leu
	110							115					120	
Met	Met	Arg	Lys	Ala	Tyr	Lys	Tyr	Ala	Phe	Asp	Lys	Tyr	Arg	Asp
	125							130					135	
Gln	Tyr	Asn	Trp	Phe	Phe	Leu	Ala	Arg	Pro	Thr	Thr	Phe	Ala	Ile
	140							145					150	
Ile	Glu	Asn	Leu	Lys	Tyr	Phe	Leu	Leu	Lys	Lys	Asp	Pro	Ser	Gln
	155							160					165	
Pro	Phe	Tyr	Leu	Gly	His	Thr	Ile	Lys	Ser	Gly	Asp	Leu	Glu	Tyr
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260

265

270

Cys Ser Asp Met Ala Val Thr Phe Asn Gly Leu Thr Pro Asn Gln  
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&lt;212&gt; PRT

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Ile	Leu	Phe	Leu	Ser	Ala	Cys	Phe	Ile	Thr	Arg	Cys	Val	Val	Thr
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Phe	Arg	Ile	Phe	Gln	Thr	Cys	Asp	Glu	Lys	Lys	Phe	Gln	Leu	Pro
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Val	Lys	Asn	Cys	Cys	Pro	Leu	Asn	Trp	Glu	Tyr	Phe	Gln	Ser	Ser
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Cys	Tyr	Phe	Phe	Ser	Thr	Asp	Thr	Ile	Ser	Trp	Ala	Leu	Ser	Leu
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Lys	Asn	Cys	Ser	Ala	Met	Gly	Ala	His	Leu	Val	Val	Ile	Asn	Ser
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Gln	Glu	Gln	Glu	Phe	Leu	Ser	Tyr	Lys	Lys	Pro	Lys	Met	Arg	
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Glu	Phe	Phe	Ile	Gly	Leu	Ser	Asp	Gln	Val	Val	Glu	Gly	Gln	Trp
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Gln	Trp	Val	Asp	Gly	Thr	Pro	Leu	Thr	Lys	Ser	Leu	Ser	Phe	Trp
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CDS/NCBI Protein Database

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Thr Cys Phe Leu Asn Tyr Phe Arg Ile Cys Glu Met Val Gly Ile  
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 ccca 3554

&lt;210&gt; 423

&lt;211&gt; 310

&lt;212&gt; PRT

&lt;213&gt; Homo Sapien

&lt;400&gt; 423

Met	Ala	Leu	Arg	Arg	Pro	Pro	Arg	Leu	Arg	Leu	Cys	Ala	Arg	Leu
1					5				10				15	

Pro	Asp	Phe	Phe	Leu	Leu	Leu	Phe	Arg	Gly	Cys	Leu	Ile	Gly
				20				25				30	

Ala	Val	Asn	Leu	Lys	Ser	Ser	Asn	Arg	Thr	Pro	Val	Val	Gln	Glu
				35				40				45		

Phe	Glu	Ser	Val	Glu	Leu	Ser	Cys	Ile	Ile	Thr	Asp	Ser	Gln	Thr
				50				55				60		

Ser	Asp	Pro	Arg	Ile	Glu	Trp	Lys	Ile	Gln	Asp	Glu	Gln	Thr
				65				70				75	

Thr	Tyr	Val	Phe	Phe	Asp	Asn	Lys	Ile	Gln	Gly	Asp	Leu	Ala	Gly
				80				85				90		

Arg	Ala	Glu	Ile	Leu	Gly	Lys	Thr	Ser	Leu	Lys	Ile	Trp	Asn	Val
				95					100			105		

Thr	Arg	Arg	Asp	Ser	Ala	Leu	Tyr	Arg	Cys	Glu	Val	Val	Ala	Arg
					110				115			120		

Asn	Asp	Arg	Lys	Glu	Ile	Asp	Glu	Ile	Val	Ile	Glu	Leu	Thr	Val
				125				130				135		

Gln	Val	Lys	Pro	Val	Thr	Pro	Val	Cys	Arg	Val	Pro	Lys	Ala	Val
				140				145				150		

Pro	Val	Gly	Lys	Met	Ala	Thr	Leu	His	Cys	Gln	Glu	Ser	Glu	Gly
				155				160				165		

His	Pro	Arg	Pro	His	Tyr	Ser	Trp	Tyr	Arg	Asn	Asp	Val	Pro	Leu
				170				175				180		

Pro	Thr	Asp	Ser	Arg	Ala	Asn	Pro	Arg	Phe	Arg	Asn	Ser	Ser	Phe
					185				190			195		

His Leu Asn Ser Glu Thr Gly Thr Leu Val Phe Thr Ala Val His  
200 205 210

Lys Asp Asp Ser Gly Gln Tyr Tyr Cys Ile Ala Ser Asn Asp Ala  
215 220 225

Gly Ser Ala Arg Cys Glu Glu Gln Glu Met Glu Val Tyr Asp Leu  
230 235 240

Asn Ile Gly Gly Ile Ile Gly Gly Val Leu Val Val Leu Ala Val  
245 250 255

Leu Ala Leu Ile Thr Leu Gly Ile Cys Cys Ala Tyr Arg Arg Gly  
260 265 270

Tyr Phe Ile Asn Asn Lys Gln Asp Gly Glu Ser Tyr Lys Asn Pro  
275 280 285

Gly Lys Pro Asp Gly Val Asn Tyr Ile Arg Thr Asp Glu Glu Gly  
290 295 300

Asp Phe Arg His Lys Ser Ser Phe Val Ile  
305 310